Methods for Treating or Preventing Infections From Coagulase-Negative Staphyl cocci

Cross-Reference to Related Applications

The present application is a divisional application of U.S. Appln. Serial No. 09/386,962, filed August 31, 1999, and claims the benefit of U.S. Provisional Applications Serial No. 60/117,119, filed January 25, 1999, and Serial No. 60/098,443, filed August 31, 1998.

Field of the Invention

The present invention is in the fields of microbiology and molecular biology and more particularly is in the field of biological products for the prevention, treatment or diagnosis of coagulase negative staphylococcal infections in man and animals.

Background of the Invention

Staphylococci are Gram-positive spherical cells, usually arranged in grape-like irregular clusters. Some are members of the normal flora of the skin and mucous membranes of humans, others cause suppuration, abscess formation, a variety of pyogenic infections, and even fatal septicemia. Pathogenic staphylococci often hemolyze blood, coagulate plasma, and produce a variety of extracellular enzymes and toxins. The most common type of food poisoning is caused by a heat-stable staphylococcal enterotoxin. The genus *Staphylococcus* has at least 30 species. The three main species of clinical importance are *Staphylococcus aureus, Staphylococcus epidermidis*, and *Staphylococcus saprophyticus. Staphylococcus aureus* is coagulase-positive, which differentiates it from the other species. *S. aureus* is a major pathogen for humans. Almost every person has some type of *S. aureus* infection during a lifetime, ranging in severity from food poisoning or minor skin infections to severe life-threatening infections.

The coagulase-negative staphylococci are normal human flora which sometimes cause infection, often associated with implanted devices, especially in very young, old and immunocompromised patients. Approximately 75% of the infections caused by coagulase-negative staphylococci are due to *S. epidermidis*.

Infections due to *Staphylococcus warneri, Staphylococcus hominis*, and other species are less common. *S. saprophyticus* is a relatively common cause of urinary tract infections in young women. The staphylococci produce catalase, which differentiates them from the streptococci.

Both *Staphylococcus aureus* and *Staphylococcus epidermidis* have a characteristic propensity for invading skin and adjacent tissues at the site of prosthetic medical devices, including intravascular catheters, cerebrospinal fluid shunts, hemodialysis shunts, vascular grafts, and extended wear contact lenses. Within 48 to 72 hours, relatively large numbers of staphylococci are demonstrable at the site of insertion of these foreign bodies. (Archer, G.L., in Remington, J.S., *et al.*, Current Clinical Topics in Infectious Diseases, McGraw-Hill, NY, 25-46, 1986.)

Staphylococcus epidermidis is a generally avirulent commensal organism of the human skin, and is the principal etiologic agent of infections of peripheral and central venous catheters, prosthetic heart valves, artificial joints, and other prosthetic devices. It has been demonstrated that *S. epidermidis* cells attach and proliferate on the inner or outer surfaces of catheters, irrespective of their composition - whether polyethylene, polyvinylchloride, polyvinylfluoride or polyester based.

Initial localized infections of indwelling medical devices can lead to more serious invasive infections such as septicemia, osteomyelitis, and endocarditis. Vascular catheters are thought to become infected when microorganisms gain access to the device, and hence the bloodstream, by migration from the skin surface down the transcutaneous portion of the catheter. In infections associated with medical devices, plastic and metal surfaces become coated with host plasma and matrix proteins such as fibrinogen, vitronectin and fibronectin shortly after implantation. *S. epidermidis* bacteremia can result in an excess hospital stay of 8 days, which is quite expensive.

Although the virulence of coagulase-negative staphylococci is enhanced in the presence of a foreign body, the microbial factors that permit these normal skin commensals to become nosocomial pathogens have not been well characterized. The ability of coagulase-negative *S. epidermidis* to adhere to these proteins is of crucial importance for initiating infection. As adherence is believed to be the critical first step in the pathogenesis of coagulase-negative staphylococcal foreign-body

infections, attention has focused on surface properties of these organisms that might mediate adherence to, and then colonization of, polymeric prosthetic materials.

A number of factors influence an organism's ability to adhere to prosthetic material. These include characteristics of the microorganism and the biomaterial, and the nature of the surrounding environment. The initial attraction between the organism and the host is influenced by nonspecific forces such as surface charge, polarity, Van der Waal forces and hydrophobic interactions. The critical stage of adherence involves specific interactions between cell surface adhesins and immobilized host proteins. To date, investigation concerning the adherence of *S. epidermidis* to biomaterials has concerned itself primarily with the role of the extracellular polysaccharide or glycocalyx, also known as slime. Despite intensive study, however, the proposed role of slime in the pathogenesis of disease or even its composition remain debated. (Drewry *et al.*, *Clin. Microbiol* 28:1292-1296, 1990) Currently, extracellular slime is thought to play a role in the later stages of adherence and persistence of infection. It may serve as an ion exchange resin to optimize a local nutritional environment, prevent penetration of antibiotics into the macro-colony or protect bacteria from phagocytic host defense cells. Peters *et al.* have shown by electron microscopy studies that extracellular polysaccharide appears in the later stages of attachment and is not present during the initial phase of adherence. (*J. Infect. Dis.*, 65146:479-482, 1982) Hogt *et al.* demonstrated that removal of the extracellular slime layer by repeated washing does not diminish the ability of *S. epidermidis* to adhere to biomaterials. (*J. Gen. Microbiol.* 129:2959-2968, 1983)

Thus far, study of exopolysaccharide has lent little to prevention of initial adherence by the bacteria. Several other studies have identified other potential adhesins of *S. epidermidis* including the polysaccharide adhesin (PS/A) observed by Tojo *et al.* (*J. Infect. Dis.* 157:713-722, 1988) and the slime associated antigen (SAA) of Christensen *et al.* (*Infect Immun*, 58:2906-2911, 1990).

It has been demonstrated that PS/A is a complex mixture of monosaccharide adhesins which blocks adherence of PS/A producing strains of *S. epidermidis*. In an animal model of endocarditis antibodies directed against PS/A were protective. However, it is not clear whether this protective effect was specific, related to anti-adhesive effects of the antibody or due to a more generalized increase in the efficiency of opsonophagocytosis of blood borne bacteria. It has been hypothesized that each adhesin functions in different stages of the adherence process with one or

more of these adhesins responsible for initial attraction while others are needed for aggregation in the macro-colonies.

Despite many studies, factors involved in the initial adherence of *S. epidermidis* to biomaterials remain largely unknown. Further unknown is a practical method for preventing the first stage of infection, adherence or adhesion. Therefore, a great need remains for the discovery and characterization of bacterial adhesin proteins and the genes that encode them.

Accordingly, it is an object of the present invention to provide cell-wall associated extracellular matrix binding proteins of coagulase-negative staphylococci.

It is a further object of the present invention to provide coagulase-negative staphylococcal surface proteins that are able to inhibit staphylococcal adhesion to the immobilized extracellular matrix or host cells present on the surface of implanted biomaterials.

It is a further object of the present invention to provide a coagulase-negative staphylococci vaccine, to generate antisera and antibodies to coagulase-negative staphylococcal proteins, and to isolate antibodies to coagulase-negative staphylococci.

It is a further object of the present invention to provide improved materials and methods for detecting and differentiating coagulase-negative staphylococcal organisms in clinical and laboratory settings.

It is a further object of the invention to provide nucleic acid probes and primers specific for coagulase-negative staphylococci.

It is a further object of the invention to provide methods for detecting, diagnosing, treating or monitoring the progress of therapy for bacterial infections that are sensitive and specific for coagulase-negative staphylococci.

These and other objects, features and advantages of the present invention will become apparent after a review of the following detailed description of the disclosed embodiments and the appended claims.

SUMMARY OF THE INVENTION

Isolated proteins from coagulase-negative staphylococci and their corresponding amino acid and nucleic acid sequences are provided. The proteins are designated SdrF, SdrG and SdrH. The DNA sequence of *sdrF* and the amino acid sequence of the protein SdrF (in bold) are shown in Fig. 2 along with their

flanking sequences. The DNA sequence of *sdrG* and the amino acid sequence of the protein SdrG (in bold) are shown in Fig. 3 along with their flanking sequences. Finally, the SdrH coding region including DNA and amino acid sequence is shown in Fig. 4.

It has also been discovered that in the A region of SdrF and SdrG there is highly conserved amino acid sequence that can be used to derive a consensus TYTFTDYVD (SEQ ID NO:16) motif. The motif can be used in multicomponent vaccines to impart broad spectrum immunity to bacterial infections, and also can be used to produce monoclonal or polyclonal antibodies that impart broad spectrum passive immunity. In an alternative embodiment, any combination of the variable sequence motif derived from the Sdr protein family, (T) (Y) (T) (F) (T) (D/N) (Y) (V) (D), can be used to impart immunity or to induce protective antibodies. The proteins, or antigenic portions thereof, are used to produce antibodies for the diagnosis of coagulase-negative staphylococcal bacterial infections or for the development of anti-coagulase-negative staphylococcal vaccines for active or passive immunization. When administered to a wound or used to coat polymeric biomaterials *in vitro* and *in vivo*, both the protein and antibodies thereof are also useful as blocking agents to prevent or inhibit the binding of coagulase-negative staphylococci to the wound site or to any biomaterials. The SdrF, SdrG and SdrH proteins are further useful as scientific research tools to understand of the mechanisms of bacterial pathology and the development of antibacterial therapies.

The *sdrF*, *sdrG* and *sdrH* gene sequences are useful as nucleic acid probes for the detection and identification of coagulase-negative staphylococcal cell surface proteins. The nucleic acid sequences may also be inserted into a vector and placed in a microorganism for the production of recombinant SdrF, SdrG and SdrH proteins. The amino acid sequences of these Sdr proteins are useful as well, for example, in the production of synthetic SdrF, SdrG and SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs.

Antisera and antibodies raised against the SdrF, SdrG and SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs, and vaccines or other pharmaceutical compositions containing the proteins are also provided herein.

In addition, diagnostic kits containing nucleic acid molecules, the proteins, antibodies or antisera raised against SdrF, SdrG and SdrH or portions thereof, such

as consensus or variable sequence amino acid motifs, and the appropriate reagents for reaction with a sample are also provided.

In a first embodiment of this invention the polynucleotide comprises a region encoding SdrF polypeptides comprising the sequence set out in Fig. 2, or a variant thereof.

In accordance with this aspect of the invention there is provided an isolated nucleic acid molecule encoding a mature polypeptide expressible by the *Staphylococcus epidermidis* strain 9491.

In a second embodiment of this invention the polynucleotide comprises a region encoding SdrG polypeptides comprising the sequence set out in Fig. 3, or a variant thereof.

In accordance with this aspect of the invention there is provided an isolated nucleic acid molecule encoding a mature polypeptide expressible by the *Staphylococcus epidermidis* strain K28.

In a third embodiment of this invention the polynucleotide comprises a region encoding SdrH polypeptides comprising the sequence set out in Fig. 4, or a variant thereof.

In accordance with this aspect of the invention there is provided an isolated nucleic acid molecule encoding a mature polypeptide expressible by the *Staphylococcus epidermidis* strain 9491.

In a fourth embodiment of the invention there is a novel protein from *Staphylococcus epidermidis* comprising the SdrF amino acid sequence as shown in Fig. 2, or a variant thereof.

In a fifth embodiment of the invention there is a novel protein from *Staphylococcus epidermidis* comprising the SdrG amino acid sequence as shown in Fig. 3, or a variant thereof.

In a sixth embodiment of the invention there is a novel protein from *Staphylococcus epidermidis* comprising the SdrH amino acid sequence as shown in Fig. 4, or a variant thereof.

In accordance with the fourth, fifth and sixth embodiments of the invention there are provided isolated nucleic acid molecules encoding SdrF, SdrG or SdrH proteins, particularly *Staphylococcus epidermidis* proteins, including mRNAs, cDNAs, genomic DNAs. Further embodiments of this aspect of the invention include

biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

In a seventh embodiment of the invention, there is provided the use of a polynucleotide of the invention for therapeutic or prophylactic purposes, in particular genetic immunization.

In an eighth embodiment of the invention are variants of SdrF, SdrG or SdrH polypeptide or portions thereof, such as consensus or variable sequence amino acid motifs, encoded by naturally occurring alleles of the *sdrF*, *sdrG* or *sdrH* gene.

In accordance with this embodiment of the invention there are provided novel polypeptides of *Staphylococcus epidermidis* referred to herein as SdrF, SdrG or SdrH or portions thereof, such as consensus or variable sequence amino acid motifs, as well as biologically, diagnostically, prophylactically, clinically or therapeutically useful variants thereof, and compositions comprising the same.

In a ninth embodiment of the invention, there are provided methods for producing the aforementioned SdrF, SdrG or SdrH polypeptides or portions thereof, such as consensus or variable sequence amino acid motifs.

In a tenth embodiment of the invention, there are provided antibodies against SdrF, SdrG or SdrH polypeptides or polynucleotides or portions thereof, such as consensus or variable sequence amino acid motifs or the nucleic acids which encode such motifs.

In an eleventh embodiment of the invention there are provided polynucleotides that hybridize to SdrF, SdrG or SdrH polynucleotide sequences or portions thereof, such as consensus or variable sequence amino acid motifs, particularly under stringent conditions.

In a twelfth embodiment of the invention there are provided compositions comprising an SdrF, SdrG or SdrH polynucleotide or a SdrF, SdrG or SdrH polypeptide or portions thereof, such as consensus or variable sequence amino acid motifs, for administration to a cell or to a multicellular organism.

Various changes and modifications within the spirit and scope of the disclosed invention will become readily apparent to those skilled in the art from reading the following descriptions and from reading the other parts of the present disclosure.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 is a representation of the SdrG protein of *S. epidermidis* strain K28. The regions are labeled along the top of the construct, with the number of amino acids found in each region of the protein disclosed immediately below the corresponding region in the drawing.

Figure 2 is the DNA sequence of *sdrF* (SEQ ID No. 1) and the amino acid sequence of the SdrF protein (in bold) along with their flanking sequences (SEQ ID Nos. 2-6).

Figure 3 is the DNA sequence of *sdrG* (SEQ ID No. 7) and the amino acid sequence of the SdrG protein (in bold) along with their flanking sequences (SEQ ID No. 8-12).

Figure 4 is the DNA sequence of the *sdrH* (SEQ ID No. 13) coding region along with the amino acid sequence of the SdrH protein (SEQ ID No. 14).

Figure 5 shows the relationships between the Sdr proteins of *S. aureus* and *S. epidermidis* as follows: Fig. 5A is a schematic representation of previously described *S. aureus* Sdr proteins; Fig. 5B is a schematic representation of SdrF, SdrG, and SdrH showing the relative position and/or size of their signal sequences (S), region As (A), region B repeats (B_n), SD-repeat region (SD), region C (C) (SdrH only), and wall/membrane spanning regions (WM); and Fig. 5C represents the C-terminal amino acid sequences of SdrF, SdrG, and SdrH showing the positions of the SD repeats, LPXTG motif (underlined), hydrophobic membrane-spanning regions (bold), and charged terminal residues.

Figure 6 illustrates the prevalence of the *sdr* genes in *S. epidermidis* strains and shows Southern blots containing *S. epidermidis* genomic DNA hybridizing to DNA probes encoding the: (A) the SD-repeat region; (B) the SdrH region A; (C) the SdrG region A; and (D) the SdrG and SdrF region As. Strains are as follows: lane 1, ATCC14990; lane 2, KH11; lane 3, K28; lane 4, RP62a; lane 5, TU3298; lane 6, 9142; lane 7 1457; lane 8, 8400; lane 9, N910308; lane 10, N910160; lane 11, N910102; lane 12, N910173; lane 13, N910191; lane 14, N910231; lane 15, N950249. Strain 9491 is not shown. Kilobases (kb) size markers are shown at the left of panels A-D.

Figure 7 shows the recombinant Sdr region A proteins and the specificity of their respective antisera as evidenced by: (A) Coomassie-stained SDS-PAGE of purified proteins used to raise rabbit polyclonal antisera. Lanes 1 and 2, histidine-tagged SdrFA and SdrGA, respectively; lane 3, GST-tagged SdrHA; (B) Left panel:

Reactivity of pooled anti-SdrFA, -SdrGA, and -SdrHA antisera to *E. coli* lysates expressing GST-tagged SdrFA (lane 1), SdrGA (lane 2), and SdrHA (lane 3). Middle and right panels: Reactivity of anti-SdrFA and -SdrGA antisera, respectively, to the same proteins; and (C) Left panel: Reactivity of anti-histidine monoclonal antibody to *E. coli* lysates expressing histidine-tagged SdrFA (lane 1), SdrGA (lane 2) and full-length SdrH (lane 3). Right panel: Reactivity of anti-SdrHA antiserum to the same proteins. Kilodalton (kDa) size markers are shown at the left of panels A, B, and C.

Figure 8 depicts immunoblot analyses of Sdr protein expression in *S. epidermidis*, including: (A) Reactivity of anti-SdrFA antisera to a lysate of *S. epidermidis* 9491. Lane 1, immune antiserum; lane 2, preimmune antiserum; and lane 3, SdrFA-absorbed immune antiserum; (B) Reactivity of anti-SdrGA immune (lane 1), preimmune (lane 2), and SdrGA-absorbed immune (lane 3) antisera to a lysate of *S. epidermidis* strain K28; and (C) Reactivity of anti-SdrHA immune (lane 1) and SdrHA-absorbed immune (lane 2) antisera to a lysate of *S. epidermidis* 9491. kDa size markers are shown to the left of A, B, and C.

Figure 9 shows the genetic analysis of SdrH protein size variation among *S. epidermidis* strains, including: (A) Reactivity of anti-SdrHA antiserum to different *S. epidermidis* strain lysates which reveal strain variations in the molecular mass of SdrH. Lane 1-3: Strains 9491, 8400, and KH11, respectively; and (B) PCR products representing DNA encoding the SdrH SD-repeat regions (lanes 1-3) or the region Cs (lanes 4-6) of the same strains. kDa and kb size markers are shown at the left of A and B, respectively.

Figure 10 represents analyses of Sdr proteins in cell-wall extracts and protoplasts, including: (A) Reactivity of anti-SdrFA antiserum to *S. epidermidis* strain 9491 lysates (lane 1), cell-wall extracts (lane 2), and purified protoplasts (lane 3); and (B) and (C) Reactivity of anti-SdrGA and -SdrHA antisera, respectively, to the same samples. KDa size markers are shown at the left of A, B, and C.

Figure 11 shows the reactivity of IgG from patients convalescing from *S. epidermidis* infections to recombinant SdrFA (open bars), SdrGA (gray bars), and SdrHA (black bars) coated in an ELISA microtiter plate. Pooled IgG from two-year-old children was used as a comparative control. Error bars reflect standard deviations.

DETAILED DESCRIPTION OF THE INVENTION

Isolated Sdr proteins and their corresponding amino acid and nucleic acid sequences are described herein. The proteins are designated SdrF, SdrG, and SdrH. The DNA sequence of *sdrF* and the amino acid sequence of the protein SdrF (in bold) are shown in Fig. 2 along with their flanking sequences. The DNA sequence of *sdrG* and the amino acid sequence of the protein SdrG (in bold) are shown in Fig. 3 along with their flanking sequences. Finally, the SdrH coding region including DNA and amino acid sequence is shown in Fig. 4.

The SdrF, SdrG, and SdrH proteins are related in primary sequence and structural organization to the extracellular matrix-binding Sdr family of proteins from *Staphylococcus aureus* and are localized on the cell surface. The SdrF, SdrG, and SdrH proteins are cell wall-associated proteins, with a signal sequence at the N-terminus and an LPXTG (SEQ ID NO:17) motif, a hydrophobic domain and positively charged residues at the C-terminus. Each also has an SD repeat containing region R of sufficient length to allow efficient expression of the ligand binding domain region A on the cell surface. With the A region of the SdrF, SdrG, and SdrH proteins located on the cell surface, the proteins can interact with proteins in plasma, the extracellular matrix or with molecules on the surface of host cells. SdrG, for example, binds the N-terminal one-half of the beta chain of fibrinogen.

The disclosed extracellular matrix-binding proteins share a unique dipeptide repeat region (region R) including predominately aspartate and serine residues. This DS repeat is encoded by 18 nucleotide repeats with the consensus GAY TCN GAY TCN GAY AGY, with TCN as the first and second serine codons and AGY as the third serine codon. The R region is near the C-terminus of the proteins and typically contains between 40 and 300 DS residues, or more particularly, greater than 60, 80, 100, 120, 150, 200 or 250 repeating units, of which greater than 90, 95 or even 98% are the amino acids D or S. The R region DS repeat varies in length between proteins, and while the region R itself does not bind extracellular matrix proteins, the R region enables the presentation of the binding regions of the protein on the cell surface of *S. aureus.* Thus, probes to the consensus DNA encoding the DS repeat (see above) can be used to identify other genes encoding different binding proteins essential to the attachment of *S. aureus* to host tissues. Antibodies to an R region can also be used to identify such additional binding proteins.

It has been discovered that in the A region of SdrF and SdrG there is highly conserved amino acid sequence that can be used to derive a consensus TYTFTDYVD (SEQ ID NO:16) motif. The motif can be used in multicomponent vaccines to impart broad spectrum immunity to bacterial infections, and also can be used to produce monoclonal or polyclonal antibodies that impart broad spectrum passive immunity. In an alternative embodiment, any combination of the variable sequence motif derived from the Sdr protein family, (T) (Y) (T) (F) (T) (D/N) (Y) (V) (D), can be used to impart immunity or to induce protective antibodies.

It has further been discovered that SdrG has an open reading frame of 2736 nucleotides that encode a protein of 913 amino acid residues. The protein has a signal sequence of 30 amino acids, a ligand binding A region of 542 amino acids, and two repeated motifs termed B regions. B1 is 113 amino acids and B2 is 110 amino acids, and the R region is 77 amino acids. B regions contain EF hand motifs that signify Ca^{++} binding, and are similar to those found in other Ca^{++} binding proteins such as calmodulin and troponin. An additional more degenerate form of the EF hand motif was found in the A region of SdrG between the residues 459-471. A significant decrease in the binding of SdrG A to Fibrinogen was noted in the presence of EDTA, demonstrating a metal-ion dependence for binding.

I. Definitions

The terms "SdrF protein", "SdrG protein" and "SdrH protein" are defined herein to include SdrF, SdrG, and SdrH subdomains, and active or antigenic fragments of SdrF, SdrG, and SdrH proteins, such as consensus or variable sequence amino acid motifs.

As used herein, "pg" means picogram, "ng" means nanogram, "ug" or "μg" mean microgram, "mg" means milligram, "ul" or "μl" mean microliter, "ml" means milliliter, "l" means liter.

"Active fragments" of SdrF, SdrG, and SdrH proteins are defined herein as peptides or polypeptides capable of blocking the binding of coagulase-negative staphylococci to immobilized or soluble host proteins.

The term "adhesin" as used herein includes naturally occurring and synthetic or recombinant proteins and peptides which can bind to extracellular matrix proteins and/or mediate adherence to host cells.

The term "amino acid" as used herein includes naturally occurring and synthetic amino acids and includes, but is not limited to, alanine, valine, leucine, isoleucine, proline, phenylalanine, tryptophan, methionine, glycine, serine, threonine, cysteine, tyrosine, asparagine, glutamate, aspartic acid, glutamic acid, lysine, arginine, and histidine.

An "antibody" is any immunoglobulin, including antibodies and fragments thereof, that binds a specific epitope. The term as used herein includes monoclonal antibodies, polyclonal, chimeric, single chain, bispecific, simianized, and humanized antibodies as well as Fab fragments, including the products of an Fab immunoglobulin expression library.

The phrase "antibody molecule" in its various grammatical forms as used herein contemplates both an intact immunoglobulin molecule and an immunologically active portion of an immunoglobulin molecule.

"Antigenic fragments" of SdrF, SdrG, and SdrH proteins are defined herein as peptides or polypeptides capable of producing an immunological response.

As used herein, an "antigenically functional equivalent" protein or peptide is one that incorporates an epitope that is immunologically cross-reactive with one or more epitopes of the particular proteins disclosed. Antigenically functional equivalents, or epitopic sequences, may be first designed or predicted and then tested, or may simply be directly tested for cross-reactivity.

A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

A "clone" is a population of cells derived from a single cell or common ancestor by mitosis.

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic MRNA, genetic DNA sequences from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

"DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in either its single stranded form, or a double stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia,* in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having a sequence homologous to the mRNA.

Transcriptional and translational control sequences are "DNA regulatory sequences", such as promoters, enhancers, polyadenylation signals, terminators, and the like, that provide for the expression of a coding sequence in a host cell.

An "expression control sequence" is a DNA sequence that controls and regulates the transcription and translation of another DNA sequence. A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then translated into the protein encoded by the coding sequence.

As used herein, the term "extracellular matrix proteins," or ECM, refers to four general families of macromolecules, collagens, structural glycoproteins, proteoglycans and elastins, including fibronectin, and fibrinogen, that provide support and modulate cellular behavior.

As used herein, a "host cell" is a cell which has been transformed or transfected, or is capable of transformation or transfection by an exogenous polynucleotide sequence.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences.

"Identity" and "similarity" can be readily calculated by known methods (Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993). While there exist a number of methods to

measure identity and similarity between two sequences, both terms are well known to skilled artisans. Methods commonly employed to determine identity or similarity between sequences include, but are not limited to those disclosed in Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48:1073 (1988). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity and similarity are codified in publicly available computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, *Nucleic Acids Research* 12(I): 387, 1984), BLASTP, BLASTN, and FASTA (Atschul *et al.*, *J. Molec. Biol.* 215: 403-410, 1990). The BLAST X program is publicly available from NCBI and other sources (BLAST Manual, Altschul *et al.*, NCBI NLM NIH Bethesda, Md. 20894; Altschul *et al.*, *J. Mol. Biol.* 215: 403-410, 1990).

By "immunologically effective amount" is meant an amount of a peptide composition that is capable of generating an immune response in the recipient animal. This includes both the generation of an antibody response (B cell response), and/or the stimulation of a cytotoxic immune response (T cell response). The generation of such an immune response will have utility in both the production of useful bioreagents, e.g., CTLs and, more particularly, reactive antibodies, for use in diagnostic embodiments, and will also have utility in various prophylactic or therapeutic embodiments.

As used herein, the term *"in vivo* vaccine" refers to immunization of animals with proteins so as to elicit a humoral and cellular response that protects against later exposure to the pathogen.

The term "isolated" is defined herein as free from at least some of the components with which it naturally occurs. "Isolated" as used herein also means altered "by the hand of man" from its natural state, i.e., if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living organism is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

The term "ligand" is used to include molecules, including those within host tissues, to which pathogenic bacteria attach.

The phrase "monoclonal antibody" in its various grammatical forms refers to an antibody having only one species of antibody combining site capable of immunoreacting with a particular antigen.

The term "oligonucleotide," as used herein is defined as a molecule comprised of two or more nucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

As used herein, the phrase "pharmaceutically acceptable" refers to molecular entities and compositions that are physiologically tolerable and do not typically produce an unacceptable allergic or similar untoward reaction when administered to a human.

"Polynucleotide(s)" generally refers to any polyribonucleotide or polydeoxyribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotide(s)" include, without limitation, single-and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions or single-, double- and triple-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, "polynucleotide" as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term "polynucleotide(s)" includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "polynucleotide(s)" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are polynucleotides as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term "polynucleotide(s)" as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of polynucleotides, as well as the chemical forms of DNA and RNA characteristic of

viruses and cells, including, for example, simple and complex cells. "Polynucleotide(s)" embraces short polynucleotides often referred to as oligonucleotide(s).

"Polypeptide(s)" refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds. "Polypeptide(s)" refers to both short chains, commonly referred to as peptides, oligopeptides and oligomers and to longer chains generally referred to as proteins. Polypeptides may contain amino acids other than the 20 genetically encoded amino acids. "Polypeptide(s)" include those modified either by natural processes, such as processing and other post-translational modifications, but also by chemical modification techniques which are well known to the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature, and they are well known to those of skill in the art. It will be appreciated that the same type of modification may be present in the same or varying degree at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formulation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. See, for instance Seifter *et al.*, *Meth. Enzymol.* 182:626-646, 1990 and Rattan *et al.*, *Ann. N.Y. Acad. Sci.* 663: 48-62, 1992. Polypeptides may be branched or cyclic, with or without branching. Cyclic, branched and branched circular polypeptides may result from post-translational natural processes and may be made by entirely synthetic methods, as well.

The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and use of the method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides.

The primers herein are selected to be substantially complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a noncomplementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, noncomplementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to hybridize therewith and thereby form the template for the synthesis of the extension product.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease SI), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters will often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

A "replicon" is a genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo;* i.e., capable of replication under its own control.

As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to bacterial enzymes, each of which cuts double-stranded DNA at or near a specific palindromic nucleotide sequence.

A "signal sequence" can be included before the coding sequence. This sequence encodes a signal peptide, N-terminal to the polypeptide, that communicates to the host cell to direct the polypeptide to the cell surface or secrete the polypeptide into the media, and this signal peptide is clipped off by the host cell before the protein leaves the cell. Signal sequences can be found associated with a variety of proteins native to prokaryotes and eukaryotes.

A cell has been "transformed" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. The transforming DNA may or may not be integrated (covalently linked) into chromosomal DNA making up the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transforming DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in which the transforming DNA has become integrated into a chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transforming DNA.

"Variant(s)" as the term is used herein, is a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide respectively, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions or truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid

sequence by one or more substitutions, additions or deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques, by direct synthesis, and by other recombinant methods known to skilled artisans.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

II. Nucleic Acid and Amino Acid Sequences

The nucleic acid sequences encoding SdrF, SdrG, and SdrH (as shown in Figs. 2-4, respectively) or portions thereof, such as consensus or variable sequence amino acid motifs, are useful for the production of recombinant proteins or as nucleic acid probes for the detection of coagulase-negative staphylococci proteins in a sample or specimen with high sensitivity and specificity. The probes can be used to detect the presence of coagulase-negative staphylococci in the sample, diagnose infection with the disease, quantify the amount of coagulase-negative staphylococci in the sample, or monitor the progress of therapies used to treat the infection. The nucleic acid and amino acid sequences can also be useful as laboratory research tools to study the organism and the disease or to develop therapies and treatments for the disease.

It will be understood by those skilled in the art that the SdrF, SdrG, or SdrH proteins are also encoded by sequences substantially similar to the nucleic acid sequences provided in the Sequence Listing. Two DNA sequences are "substantially similar" when approximately 70% or more (preferably at least about 80%, and most preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, 1982; DNA Cloning, Vols. I & II,

supra; Nucleic Acid Hybridization, [B.D. Hames & S.J. Higgins eds. (1985)]. By "substantially similar" is further meant a DNA sequence which, by virtue of the degeneracy of the genetic code, is not identical with that shown in any of the sequences shown in Figs. 2-4, but which still encodes the same amino acid sequence; or a DNA sequence which encodes a different amino acid sequence that retains the activities of the proteins, either because one amino acid is replaced with a similar amino acid, or because the change (whether it be substitution, deletion or insertion) does not affect the active site of the protein. Two amino acid sequences or two nucleic acid sequences are "substantially similar" when approximately 70% or more (preferably at least about 80%, and more preferably at least about 90% or 95%) of the amino acids match over the defined length of the sequences.

Modification and changes may be made in the structure of the peptides of the present invention and DNA segments which encode them and still obtain a functional molecule that encodes a protein or peptide with desirable characteristics. The following is a discussion based upon changing the amino acids of a protein to create an equivalent, or even an improved, second generation molecule. The amino acid changes may be achieved by changing the codons of the DNA sequence, according to Table 1. It should be understood by one skilled in the art that the codons specified in Table 1 are for RNA sequences. The corresponding codons for DNA have a T substituted for U. In keeping with standard nomenclature (*J. Biol. Chem.*, 243:3552-3559, 1969), abbreviations for amino acid residues are further shown in Table 1.

Table 1

Amino Acids			Codons			
Alanine	Ala	A	GCA	GCC	GCG	GCU
Cysteine	Cys	C	UGC	UGU		
Aspartic acid	Asp	D	GAC	GAU	GAC	GAU
Glutamic acid	Glu	E	GAA	GAG		
Phenylalanine	Phe	F	UUC	UUU		
Glycine	Gly	G	GGA	GCG	GGG	GGU
Histidine	His	H	CAC	CAU		
Isoleucine	Ile	I	AUA	AUC	AUU	

Lysine	Lys	K	AAA	AAG				
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	GUU
Methionine	Met	M	AUG					
Asparagine	Asn	N	AAC	AAU				
Proline	Pro	P	CCA	CCC	CCG	CCU		
Glutamine	Gln	Q	CAA	CAG				
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU
Threonine	Thr	T	ACA	ACC	ACG	ACU		
Valine	Val	V	GUA	GUC	GUG	GUU		
Tryptophan	Trp	W	UGG					
Tyrosine	Tyr	Y	UAC	UAU				

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, *J. Mol Biol*, 157(1):105-132, 1982, incorporate herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, *supra,* 1982), these are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (-0.4); threonine (-0.7); serine (-0.8); tryptophan (-0.9); tyrosine (-1.3); proline (-1.6); histidine (-3.2); glutamate (-3.5); glutamine (-3.5); aspartate (-3.5); asparagine (-3.5); lysine (-3.9); and arginine (-4.5).

It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, i.e., still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those which are within ±l are particularly preferred, and those within ±0.5 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as governed by the

hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+1.0); aspartate (+3.0 ± 1); glutamate (+3.0 ± 1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (-0.4); proline (-0.5 ± 1); alanine (-0.5); histidine (-0.5); cysteine (-1.0); methionine (-1.3); valine (-1.5); leucine (-1.8); isoleucine (-1.8); tyrosine (-2.3); phenylalanine (-2.5); tryptophan (-3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those which are within ±l are particularly preferred, and those within ±0.5 are even more particularly preferred.

As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions which take various of the foregoing characteristics into consideration are well known to those of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

The polypeptides of the present invention can be can be chemically synthesized. The synthetic polypeptides are prepared using the well known techniques of solid phase, liquid phase, or peptide condensation techniques, or any combination thereof, and can include natural and unnatural amino acids. Amino acids used for peptide synthesis may be standard Boc (N^a-amino protected N^a-t-butyloxycarbonyl) amino acid resin with the standard deprotecting, neutralization, coupling and wash protocols of the original solid phase procedure of Merrifield (*J. Am. Chem. Soc.,* 85:2149-2154, 1963), or the base-labile N^a-amino protected 9-fluorenylmethoxycarbonyl (Fmoc) amino acids first described by Carpino and Han (*J. Org. Chem.,* 37:3403-3409, 1972). Both Fmoc and Boc N^a-amino protected amino acids can be obtained from Fluka, Bachem, Advanced Chemtech, Sigma, Cambridge Research Biochemical, Bachem, or Peninsula Labs or other chemical companies familiar to those who practice this art. In addition, the method of the invention can be used with other N^a-protecting groups that are familiar to those skilled in this art. Solid phase peptide synthesis may be accomplished by techniques

familiar to those in the art and provided, for example, in Stewart and Young, 1984, Solid Phase Synthesis, Second Edition, Pierce Chemical Co., Rockford, IL; Fields and Noble, 1990, *Int. J. Pept Protein Res.* 35:161-214, or using automated synthesizers, such as sold by ABS. Thus, polypeptides of the invention may comprise D-amino acids, a combination of D- and L-amino acids, and various "designer" amino acids (*e.g.*, β-methyl amino acids, Cα-methyl amino acids, and Nα-methyl amino acids, etc.) to convey special properties. Synthetic amino acids include ornithine for lysine, fluorophenylalanine for phenylalanine, and norleucine for leucine or isoleucine. Additionally, by assigning specific amino acids at specific coupling steps, α-helices, β turns, β sheets, γ-turns, and cyclic peptides can be generated.

In a further embodiment, subunits of peptides that confer useful chemical and structural properties will be chosen. For example, peptides comprising D-amino acids will be resistant to L-amino acid-specific proteases *in vivo*. In addition, the present invention envisions preparing peptides that have more well defined structural properties, and the use of peptidomimetics and peptidomimetic bonds, such as ester bonds, to prepare peptides with novel properties. In another embodiment, a peptide may be generated that incorporates a reduced peptide bond, i.e., R_1-CH_2-NH-R_2, where R_1 and R_2 are amino acid residues or sequences. A reduced peptide bond may be introduced as a dipeptide subunit. Such a molecule would be resistant to peptide bond hydrolysis, *e.g.*, protease activity. Such peptides would provide ligands with unique function and activity, such as extended half-lives *in vivo* due to resistance to metabolic breakdown or protease activity. Furthermore, it is well known that in certain systems constrained peptides show enhanced functional activity (Hruby, *Life Sciences,* 31:189-199, 1982); (Hruby *et al., Biochem J.,* 268:249-262, 1990).

The following non-classical amino acids may be incorporated in the peptide in order to introduce particular conformational motifs: 1,2,3,4-tetrahydroisoquinoline-3--carboxylate (Kazmierski *et al., J. Am. Chem. Soc.,* 113:2275-2283, 1991); (2S,3S)-methyl-phenylalanine, (2S,3R)-methyl-phenylalanine, (2R,3S)-methyl-phenylalanine and (2R,3R)-methyl-phenylalanine (Kazmierski and Hruby, *Tetrahedron Lett.,* 1991); 2-aminotetrahydronaphthalene-2-carboxylic acid (Landis, *Ph.D. Thesis, University of Arizona,* 1989); hydroxy-1,2,3,4-tetrahydro-isoquinoline-3-carboxylate (Miyake *et al, J. Takeda Res. Labs.,* 43:53-76, 1989);

β-carboline (D and L) (Kazmierski, *Ph.D. Thesis, University of Arizona,* 1988); HIC (histidine isoquinoline carboxylic acid) (Zechel *et al, Int. J. Pep. Protein Res.,* 43, 1991); and HIC (histidine cyclic urea) (Dharanipragada).

The following amino acid analogs and peptidomimetics may be incorporated into a peptide to induce or favor specific secondary structures: LL-Acp (LL-3-amino-2-propenidone-6-carboxylic acid), a β-turn inducing dipeptide analog (Kemp *et al.,* J. *Org. Chem.,* 50:5834-5838 (1985); β-sheet inducing analogs (Kemp *et al., Tetrahedron Lett.,* 29:5081-5082, 1988); β-turn inducing analogs (Kemp *et al., Tetrahedron Lett.,* 29:5057-5060, 1988); alpha-helix inducing analogs (Kemp *et al., Tetrahedron Lett.,* 29:4935-4938, 1988); γ-turn inducing analogs (Kemp *et al.,* J. *Org. Chem.,* 54:109:115, 1989); and analogs provided by the following references: Nagai and Sato, *Tetrahedron Lett.,* 26:647-650 (1985); DiMaio *et al.*, J. Chem. Soc. *Perkin Trans.,* p. 1687 (1989); also a Gly-Ala turn analog (Kahn *et al., Tetrahedron Lett.,* 30:2317, 1989); amide bond isostere (Jones *et al., Tetrahedron Lett.,* 29:3853-3856, 1989); tetrazole (Zabrocki *et al., J. Am. Chem. Soc.,* 110:5875-5880, 1988); DTC (Samanen *et al., Int. J. Protein Pep. Res.,* 35:501:509, 1990); and analogs taught in Olson *et al., (J. Am. Chem. Sci.,* 112:323-333, 1990) and Garvey *et al.,(J. Org. Chem.,* 56:436, 1990). Conformationally restricted mimetics of beta turns and beta bulges, and peptides containing them, are described in U.S. Patent No. 5,440,013, issued August 8, 1995 to Kahn.

Also provided herein are sequences of nucleic acid molecules that selectively hybridize with nucleic acid molecules encoding the fibrinogen-binding proteins or portions thereof, such as consensus or variable sequence amino acid motifs, from coagulase-negative staphylococcal bacteria such as *S. epidermidis* described herein or complementary sequences thereof. By "selective" or "selectively" is meant a sequence which does not hybridize with other nucleic acids. This is to promote specific detection of *sdrF*, *sdrG*, or *sdrH*. Therefore, in the design of hybridizing nucleic acids, selectivity will depend upon the other components present in a sample. The hybridizing nucleic acid should have at least 70% complementarity with the segment of the nucleic acid to which it hybridizes. As used herein to describe nucleic acids, the term "selectively hybridizes" excludes the occasional randomly hybridizing nucleic acids, and thus, has the same meaning as "specifically hybridizing". The selectively hybridizing nucleic acids of the invention can have at

least 70%, 80%, 85%, 90%, 95%, 97%, 98%, and 99% complementarity with the segment of the sequence to which they hybridize.

The invention contemplates sequences, probes and primers which selectively hybridize to the encoding DNA or the complementary, or opposite, strand of DNA as those specifically provided herein. Specific hybridization with nucleic acid can occur with minor modifications or substitutions in the nucleic acid, so long as functional species-specific hybridization capability is maintained. By "probe" is meant nucleic acid sequences that can be used as probes or primers for selective hybridization with complementary nucleic acid sequences for their detection or amplification, which probes can vary in length from about 5 to 100 nucleotides, or preferably from about 10 to 50 nucleotides, or most preferably about 18-24 nucleotides. Therefore, the terms "probe" or "probes" as used herein are defined to include "primers". Isolated nucleic acids are provided herein that selectively hybridize with the species-specific nucleic acids under stringent conditions and should have at least 5 nucleotides complementary to the sequence of interest as described by Sambrook *et al.*, 1989. MOLECULAR CLONING: A LABORATORY MANUAL, 2nd ed. Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.

If used as primers, the composition preferably includes at least two nucleic acid molecules which hybridize to different regions of the target molecule so as to amplify a desired region. Depending on the length of the probe or primer, the target region can range between 70% complementary bases and full complementarity and still hybridize under stringent conditions. For example, for the purpose of diagnosing the presence of the *S. epidermidis*, the degree of complementarity between the hybridizing nucleic acid (probe or primer) and the sequence to which it hybridizes (e.g., coagulase-negative staphylococcal DNA from a sample) is at least enough to distinguish hybridization with a nucleic acid from other bacteria.

The nucleic acid sequences encoding SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs, can be inserted into a vector, such as a plasmid, and recombinantly expressed in a living organism to produce recombinant SdrF, SdrG, or SdrH proteins or fragments thereof. For example, DNA molecules producing recombinant SdrF, SdrG, and SdrH have been produced in plasmids in accordance with the present invention.

Recombinant proteins are produced by methods well known to those skilled in the art. A cloning vector, such as a plasmid or phage DNA is cleaved with a

restriction enzyme, and the DNA sequence encoding the SdrF, SdrG, or SdrH protein or fragments thereof, such as consensus or variable sequence amino acid motifs, is inserted into the cleavage site and ligated. The cloning vector is then inserted into a host to produce the protein or fragment encoded by the SdrF, SdrG, or SdrH encoding DNA. Suitable hosts include bacterial hosts such as *Escherichia coli*, *Bacillus subtilis*, yeasts and other cell cultures. Production and purification of the gene product may be achieved and enhanced using known molecular biology techniques.

III. Uses of *sdr* nucleic acids

Methods of using the nucleic acids described herein to detect and identify the presence of coagulase-negative staphylococci are provided. The methods are useful for diagnosing coagulase-negative staphylococcal infections and other associated diseases such as catheter related infections, biomaterial related infections, upper respiratory tract infections (such as otitis media, bacterial tracheitis, acute epiglottitis, thyroiditis), lower respiratory infections (such as emphysema, lung abscess), cardiac (such as infective endocarditis), gastrointestinal (such as secretory diarrhea, splenic abscess, retroperitoneal abscess), central nervous system (such as cerebral abscess), ocular (such as blepharitis, conjunctivitis, keratitis, endophthalmitis, preseptal and orbital cellulitis, darcryocystitis), kidney and urinary tract (such as epididymitis, intrarenal and perinephric abscess, toxic shock syndrome), skin (such as impetigo, folliculitis, cutaneous abscesses, cellulitis, wound infection, bacterial myositis, bone and joint (such as septic arthritis, osteomyelitis), bovine mastitis, and canine pyoderma.

The method involves the steps of obtaining a sample suspected of containing coagulase-negative staphylococci. The sample may be taken from an individual, for example, from one's blood, saliva, tissues, bone, muscle, cartilage, or skin. The cells can then be lysed, and the DNA extracted, precipitated and amplified. Detection of DNA from coagulase-negative staphylococci is achieved by hybridizing the amplified DNA with a probe for coagulase-negative staphylococci that selectively hybridizes with the DNA as described above in the Detailed Description of the Invention. Detection of hybridization is indicative of the presence of coagulase-negative staphylococci.

Preferably, detection of nucleic acid (e.g. probes or primers) hybridization can be facilitated by the use of detectable moieties. For example, the probes can be labeled with biotin and used in a streptavidin-coated microtiter plate assay. Other detectable moieties include radioactive labeling, enzyme labeling, and fluorescent labeling, for example.

DNA may be detected directly or may be amplified enzymatically using polymerase chain reaction (PCR) or other amplification techniques prior to analysis. RNA or cDNA can be similarly detected. Increased or decrease expression of *sdrF*, *sdrG*, or *sdrH* can be measured using any of the methods well known in the art for the quantification of nucleic acid molecules, such as, for example, amplification, PCR, RT-PCR, RNase protection, Northern blotting, and other hybridization methods.

Diagnostic assays for SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs, or anti- SdrF, SdrG, or SdrH antibodies may also be used to detect the presence of a *Staphylococcus epidermidis* infection. Assay techniques for determining protein or antibody levels in a sample are well known to those skilled in the art and include methods such as radioimmunoasssay, Western blot analysis and ELISA assays.

IV. Uses of Sdr Protein or Antibody

The isolated, recombinant or synthetic proteins, or antigenic portions thereof (including epitope-bearing fragments), or fusion proteins thereof can be administered to animals as immunogens or antigens, alone or in combination with an adjuvant, for the production of antibodies reactive with SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs. In addition, the proteins can be used to screen antibodies or antisera for hyperimmune patients from whom can be derived specific antibodies having a very high affinity for the proteins.

Antibodies to SdrF, SdrG, or SdrH or to fragments thereof, such as consensus or variable sequence amino acid motifs, can be used to impart passive immunity are useful for the specific detection of coagulase-negative staphylococci proteins, for the prevention of a coagulase-negative staphylococcal infection, for the treatment of an ongoing infection or for use as research tools. The term "antibodies" as used herein includes monoclonal, polyclonal, chimeric, single chain, bispecific, simianized, and humanized or primatized antibodies as well as Fab fragments, including the products

of an Fab immunoglobulin expression library. Generation of any of these types of antibodies or antibody fragments is well known to those skilled in the art.

Monoclonal antibodies are generated by methods well known to those skilled in the art. The preferred method is a modified version of the method of Kearney *et al.*, *J. Immunol.* 123:1548-1558 (1979), which is incorporated by reference herein. Briefly, animals such as mice or rabbits are inoculated with the immunogen in adjuvant, and spleen cells are harvested and mixed with a myeloma cell line, such as P3X63Ag8,653. The cells are induced to fuse by the addition of polyethylene glycol. Hybridomas are chemically selected by plating the cells in a selection medium containing hypoxanthine, aminopterin and thymidine (HAT). Hybridomas are subsequently screened for the ability to produce anti-SdrF, SdrG, or SdrH monoclonal antibodies. Hybridomas producing antibodies are cloned, expanded and stored frozen for future production.

Techniques for the production of single chain antibodies are known to those skilled in the art and described in U.S. Patent No. 4,946,778 and can be used to produce single chain antibodies to the proteins described herein. Phage display technology may be used to select antibody genes having binding activities for SdrF, SdrG, or SdrH, or antigenic portions thereof, such as consensus or variable sequence amino acid motifs, from PCR-amplified genes of lymphocytes from humans screened for having antibodies to SdrF, SdrG, or SdrH or naive libraries. Bispecific antibodies have two antigen binding domains wherein each domain is directed against a different epitope.

Any of the above described antibodies may be labeled directly with a detectable label for identification and quantification of coagulase-negative staphylococci. Labels for use in immunoassays are generally known to those skilled in the art and include enzymes, radioisotopes, and fluorescent, luminescent and chromogenic substances, including colored particles such as colloidal gold or latex beads. Suitable immunoassays include enzyme-linked immunosorbent assays (ELISA).

Alternatively, the antibody may be labeled indirectly by reaction with labeled substances that have an affinity for immunoglobulin. The antibody may be conjugated with a second substance and detected with a labeled third substance having an affinity for the second substance conjugated to the antibody. For example, the antibody may be conjugated to biotin and the antibody-biotin conjugate

detected using labeled avidin or streptavidin. Similarly, the antibody may be conjugated to a hapten and the antibody-hapten conjugate detected using labeled anti-hapten antibody. These and other methods of labeling antibodies and assay conjugates are well known to those skilled in the art.

Antibodies to the extracellular matrix-binding proteins SdrF, SdrG, SdrH or portions thereof, such as consensus or variable sequence amino acid motifs, may also be used in production facilities or laboratories to isolate additional quantities of the proteins, such as by affinity chromatography. For example, antibodies to the fibrinogen-binding protein SdrG may be used to isolate additional amounts of fibrinogen.

The proteins, or active fragments thereof, and antibodies to the proteins are useful for the treatment and diagnosis of coagulase-negative staphylococci bacterial infections as described above with regard to diagnosis method, or for the development of anti-coagulase-negative staphylococci vaccines for active or passive immunization. Further, when administered as pharmaceutical composition to a wound or used to coat medical devices or polymeric biomaterials *in vitro* and *in vivo*, both the proteins and the antibodies are useful as blocking agents to prevent or inhibit the binding of coagulase-negative staphylococci to the wound site or the biomaterials themselves. Preferably, the antibody is modified so that it is less immunogenic in the patient to whom it is administered. For example, if the patient is a human, the antibody may be "humanized" by transplanting the complimentarity determining regions of the hybridoma-derived antibody into a human monoclonal antibody as described by Jones *et al.*, *Nature* 321:522-525 (1986) or Tempest *et al. Biotechnology* 9:266-273 (1991) and as mentioned above.

Medical devices or polymeric biomaterials to be coated with the antibodies, proteins and active fragments described herein include, but are not limited to, staples, sutures, replacement heart valves, cardiac assist devices, hard and soft contact lenses, intraocular lens implants (anterior chamber or posterior chamber), other implants such as corneal inlays, kerato-prostheses, vascular stents, epikeratophalia devices, glaucoma shunts, retinal staples, scleral buckles, dental prostheses, thyroplastic devices, laryngoplastic devices, vascular grafts, soft and hard tissue prostheses including, but not limited to, pumps, electrical devices including stimulators and recorders, auditory prostheses, pacemakers, artificial larynx, dental implants, mammary implants, penile implants, cranio/facial tendons,

artificial joints, tendons, ligaments, menisci, and disks, artificial bones, artificial organs including artificial pancreas, artificial hearts, artificial limbs, and heart valves; stents, wires, guide wires, intravenous and central venous catheters, laser and balloon angioplasty devices, vascular and heart devices (tubes, catheters, balloons), ventricular assists, blood dialysis components, blood oxygenators, urethral/ureteral/urinary devices (Foley catheters, stents, tubes and balloons), airway catheters (endotracheal and tracheostomy tubes and cuffs), enteral feeding tubes (including nasogastric, intragastric and jejunal tubes), wound drainage tubes, tubes used to drain the body cavities such as the pleural, peritoneal, cranial, and pericardial cavities, blood bags, test tubes, blood collection tubes, vacutainers, syringes, needles, pipettes, pipette tips, and blood tubing.

It will be understood by those skilled in the art that the term "coated" or "coating", as used herein, means to apply the protein, antibody, or active fragment to a surface of the device, preferably an outer surface that would be exposed to coagulase-negative staphylococcal infection. The surface of the device need not be entirely covered by the protein, antibody or active fragment.

V. Pharmaceutical Compositions

Immunological compositions, including vaccines, and other pharmaceutical compositions containing the SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs, are included within the scope of the present invention. One or more of the SdrF, SdrG, or SdrH proteins, or active or antigenic fragments thereof, or fusion proteins thereof can be formulated and packaged, alone or in combination with other antigens, using methods and materials known to those skilled in the art for vaccines. The immunological response may be used therapeutically or prophylactically and may provide antibody immunity or cellular immunity, such as that produced by T lymphocytes.

The immunological compositions, such as vaccines, and other pharmaceutical compositions can be used alone or in combination with other blocking agents to protect against human and animal infections caused by or exacerbated by coagulase-negative staphylococci. In particular, the compositions can be used to protect humans against endocarditis, toxic shock syndrome, osteomyelitis, epididymitis, cellulitis or many other infections. The compositions may also protect humans or ruminants against mastitis caused by coagulase-negative staphylococci

infections. The vaccine can further be used to protect other species of animals, for example canine and equine animals, against similar coagulase-negative staphylococcal infections.

To enhance immunogenicity, the proteins may be conjugated to a carrier molecule. Suitable immunogenic carriers include proteins, polypeptides or peptides such as albumin, hemocyanin, thyroglobulin and derivatives thereof, particularly bovine serum albumin (BSA) and keyhole limpet hemocyanin (KLH), polysaccharides, carbohydrates, polymers, and solid phases. Other protein derived or non-protein derived substances are known to those skilled in the art. An immunogenic carrier typically has a molecular mass of at least 1,000 Daltons, preferably greater than 10,000 Daltons. Carrier molecules often contain a reactive group to facilitate covalent conjugation to the hapten. The carboxylic acid group or amine group of amino acids or the sugar groups of glycoproteins are often used in this manner. Carriers lacking such groups can often be reacted with an appropriate chemical to produce them. Preferably, an immune response is produced when the immunogen is injected into animals such as mice, rabbits, rats, goats, sheep, guinea pigs, chickens, and other animals, most preferably mice and rabbits. Alternatively, a multiple antigenic peptide comprising multiple copies of the protein or polypeptide, or an antigenically or immunologically equivalent polypeptide may be sufficiently antigenic to improve immunogenicity without the use of a carrier.

The SdrF, SdrG, or SdrH protein or portions thereof, such as consensus or variable sequence amino acid motifs, or combination of proteins may be administered with an adjuvant in an amount effective to enhance the immunogenic response against the conjugate. At this time, the only adjuvant widely used in humans has been alum (aluminum phosphate or aluminum hydroxide). Saponin and its purified component Quil A, Freund's complete adjuvant and other adjuvants used in research and veterinary applications have toxicities which limit their potential use in human vaccines. However, chemically defined preparations such as muramyl dipeptide, monophosphoryl lipid A, phospholipid conjugates such as those described by Goodman-Snitkoff *et al. J. Immunol.* 147:410-415 (1991) and incorporated by reference herein, encapsulation of the conjugate within a proteoliposome as described by Miller *et al., J. Exp. Med.* 176:1739-1744 (1992) and incorporated by reference herein, and encapsulation of the protein in lipid vesicles such as

Novasome™ lipid vesicles (Micro Vescular Systems, Inc., Nashua, NH) may also be useful.

The term "vaccine" as used herein includes DNA vaccines in which the nucleic acid molecule encoding SdrF, SdrG, or SdrH, or antigenic portions thereof, such as any consensus or variable sequence amino acid motif, in a pharmaceutical composition is administered to a patient. For genetic immunization, suitable delivery methods known to those skilled in the art include direct injection of plasmid DNA into muscles (Wolff *et al., Hum. Mol. Genet.* 1:363, 1992), delivery of DNA complexed with specific protein carriers (Wu *et al.*, *J. Biol. Chem.* 264:16985, 1989), coprecipitation of DNA with calcium phosphate (Benvenisty and Reshef, *Proc. Natl. Acad. Sci.* 83:9551, 1986), encapsulation of DNA in liposomes (Kaneda *et al.*, *Science* 243:375, 1989), particle bombardment (Tang *et al.*, *Nature* 356:152, 1992 and Eisenbraun *et al.*, *DNA Cell Biol.* 12:791, 1993), and *in vivo* infection using cloned retroviral vectors (Seeger *et al.*, *Proc. Natl. Acad. Sci.* 81:5849, 1984).

In another embodiment, the invention is a polynucleotide which comprises contiguous nucleic acid sequences capable of being expressed to produce a gene product upon introduction of said polynucleotide into eukaryotic tissues *in vivo*. The encoded gene product preferably either acts as an immunostimulant or as an antigen capable of generating an immune response. Thus, the nucleic acid sequences in this embodiment encode an immunogenic epitope, and optionally a cytokine or a T-cell costimulatory element, such as a member of the B7 family of proteins.

There are several advantages to immunization with a gene rather than its gene product. The first is the relative simplicity with which native or nearly native antigen can be presented to the immune system. Mammalian proteins expressed recombinantly in bacteria, yeast, or even mammalian cells often require extensive treatment to ensure appropriate antigenicity. A second advantage of DNA immunization is the potential for the immunogen to enter the MHC class I pathway and evoke a cytotoxic T cell response. Immunization of mice with DNA encoding the influenza A nucleoprotein (NP) elicited a $CD8^+$ response to NP that protected mice against challenge with heterologous strains of flu. (Montgomery, D. L. *et al.*, *Cell Mol Biol*, 43(3):285-92, 1997 and Ulmer, J. *et al.*, *Vaccine*, 15(8):792-794, 1997.)

Cell-mediated immunity is important in controlling infection. Since DNA immunization can evoke both humoral and cell-mediated immune responses, its

greatest advantage may be that it provides a relatively simple method to survey a large number of *S. epidermidis* genes for their vaccine potential.

VI. M thods of Administration and Dosage of Pharmaceutical Compositions

Pharmaceutical compositions containing the SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs, nucleic acid molecules, antibodies, or fragments thereof may be formulated in combination with a pharmaceutical carrier such as saline, dextrose, water, glycerol, ethanol, other therapeutic compounds, and combinations thereof. The formulation should be appropriate for the mode of administration. The compositions are useful for interfering with, modulating, or inhibiting binding interactions between coagulase-negative staphylococci and fibrinogen on host cells.

The amount of expressible DNA or transcribed RNA to be introduced into a vaccine recipient will have a very broad dosage range and may depend on the strength of the transcriptional and translational promoters used. In addition, the magnitude of the immune response may depend on the level of protein expression and on the immunogenicity of the expressed gene product. In general, effective dose ranges of about 1 ng to 5 mg, 100 ng to 2.5 mg, 1 μg to 750 μg, and preferably about 10 μg to 300 μg of DNA is administered directly into muscle tissue. Subcutaneous injection, intradermal introduction, impression through the skin, and other modes of administration such as intraperitoneal, intravenous, or inhalation delivery are also suitable. It is also contemplated that booster vaccinations may be provided. Following vaccination with a polynucleotide immunogen, boosting with protein immunogens such as the SdrH gene product is also contemplated.

The polynucleotide may be "naked", that is, unassociated with any proteins, adjuvants or other agents which affect the recipient's immune system. In this case, it is desirable for the polynucleotide to be in a physiologically acceptable solution, such as, but not limited to, sterile saline or sterile buffered saline. Alternatively, the DNA may be associated with liposomes, such as lecithin liposomes or other liposomes known in the art, as a DNA-liposome mixture, or the DNA may be associated with an adjuvant known in the art to boost immune responses, such as a protein or other carrier. Agents which assist in the cellular uptake of DNA, such as, but not limited to, calcium ions, may also be used. These agents are generally referred to herein as transfection facilitating reagents and pharmaceutically acceptable carriers.

Techniques for coating microprojectiles coated with polynucleotide are known in the art and are also useful in connection with this invention. For DNA intended for human use it may be useful to have the final DNA product in a pharmaceutically acceptable carrier or buffer solution. Pharmaceutically acceptable carriers or buffer solutions are known in the art and include those described in a variety of texts such as Remington's Pharmaceutical Sciences.

It is recognized by those skilled in the art that an optimal dosing schedule for a DNA vaccination regimen may include as many as five to six, but preferably three to five, or even more preferably one to three administrations of the immunizing entity given at intervals of as few as two to four weeks, to as long as five to ten years, or occasionally at even longer intervals.

Suitable methods of administration of any pharmaceutical composition disclosed in this application include, but are not limited to, topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal and intradermal administration.

For topical administration, the composition is formulated in the form of an ointment, cream, gel, lotion, drops (such as eye drops and ear drops), or solution (such as mouthwash). Wound or surgical dressings, sutures and aerosols may be impregnated with the composition. The composition may contain conventional additives, such as preservatives, solvents to promote penetration, and emollients. Topical formulations may also contain conventional carriers such as cream or ointment bases, ethanol, or oleyl alcohol.

In a preferred embodiment, a vaccine is packaged in a single dosage for immunization by parenteral (i.e., intramuscular, intradermal or subcutaneous) administration or nasopharyngeal (i.e., intranasal) administration. The vaccine is most preferably injected intramuscularly into the deltoid muscle. The vaccine is preferably combined with a pharmaceutically acceptable carrier to facilitate administration. The carrier is usually water or a buffered saline, with or without a preservative. The vaccine may be lyophilized for resuspension at the time of administration or in solution.

Microencapsulation of the protein will give a controlled release. A number of factors contribute to the selection of a particular polymer for microencapsulation. The reproducibility of polymer synthesis and the microencapsulation process, the cost of the microencapsulation materials and process, the toxicological profile, the

requirements for variable release kinetics and the physicochemical compatibility of the polymer and the antigens are all factors that must be considered. Examples of useful polymers are polycarbonates, polyesters, polyurethanes, polyorthoesters, polyamides, poly (D,L-lactide-co-glycolide) (PLGA) and other biodegradable polymers. The use of PLGA for the controlled release of antigen is reviewed by Eldridge et al., CURRENT TOPICS IN MICROBIOLOGY AND IMMUNOLOGY, 146:59-66 (1989).

The preferred dose for human administration is from 0.01 mg/kg to 10 mg/kg, preferably approximately 1 mg/kg. Based on this range, equivalent dosages for heavier body weights can be determined. The dose should be adjusted to suit the individual to whom the composition is administered and will vary with age, weight and metabolism of the individual. The vaccine may additionally contain stabilizers or pharmaceutically acceptable preservatives, such as thimerosal (ethyl(2-mercaptobenzoate-S)mercury sodium salt) (Sigma Chemical Company, St. Louis, MO).

VII. Protein-Label Conjugates

When labeled with a detectable biomolecule or chemical, the fibrinogen-binding proteins described herein are useful for purposes such as *in vivo* and *in vitro* diagnosis of staphylococcal infections or detection of coagulase-negative staphylococci. Laboratory research may also be facilitated through use of such Sdr protein-label conjugates. Various types of labels and methods of conjugating the labels to the proteins are well known to those skilled in the art. Several specific labels are set forth below. The labels are particularly useful when conjugated to a protein such as an antibody or receptor.

For example, the protein can be conjugated to a radiolabel such as, but not restricted to, ^{32}P, ^{3}H, ^{14}C, ^{35}S, ^{125}I, or ^{131}I. Detection of a label can be by methods such as scintillation counting, gamma ray spectrometry or autoradiography.

Bioluminescent labels, such as derivatives of firefly luciferin, are also useful. The bioluminescent substance is covalently bound to the protein by conventional methods, and the labeled protein is detected when an enzyme, such as luciferase, catalyzes a reaction with ATP causing the bioluminescent molecule to emit photons of light.

Fluorogens may also be used to label proteins. Examples of fluorogens include fluorescein and derivatives, phycoerythrin, allo-phycocyanin, phycocyanin, rhodamine, and Texas Red. The fluorogens are generally detected by a fluorescence detector.

The protein can alternatively be labeled with a chromogen to provide an enzyme or affinity label. For example, the protein can be biotinylated so that it can be utilized in a biotin-avidin reaction, which may also be coupled to a label such as an enzyme or fluorogen. For example, the protein can be labeled with peroxidase, alkaline phosphatase or other enzymes giving a chromogenic or fluorogenic reaction upon addition of substrate. Additives such as 5-amino-2,3-dihydro-1,4-phthalazinedione (also known as Luminol®) (Sigma Chemical Company, St. Louis, MO) and rate enhancers such as p-hydroxybiphenyl (also known as p-phenylphenol) (Sigma Chemical Company, St. Louis, MO) can be used to amplify enzymes such as horseradish peroxidase through a luminescent reaction; and luminogeneic or fluorogenic dioxetane derivatives of enzyme substrates can also be used. Such labels can be detected using enzyme-linked immunoassays (ELISA) or by detecting a color change with the aid of a spectrophotometer. In addition, proteins may be labeled with colloidal gold for use in immunoelectron microscopy in accordance with methods well known to those skilled in the art.

The location of a ligand in cells can be determined by labeling an antibody as described above and detecting the label in accordance with methods well known to those skilled in the art, such as immunofluorescence microscopy using procedures such as those described by Warren and Nelson (*Mol. Cell. Biol.,* 7: 1326-1337, 1987).

VIII. Therapeutic Applications

In addition to the therapeutic compositions and methods described above, the SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs, nucleic acid molecules or antibodies are useful for interfering with the initial physical interaction between a pathogen and mammalian host responsible for infection, such as the adhesion of bacteria, particularly Gram-negative bacteria, to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in wounds; to block SdrF, SdrG, or SdrH protein-mediated mammalian cell invasion; to block bacterial adhesion between mammalian

extracellular matrix proteins and bacterial SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs, that mediate tissue damage; and, to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or surgical techniques.

IX. Screening Methods

The SdrF, SdrG, or SdrH proteins, or fragments thereof, such as consensus or variable sequence amino acid motifs, are useful in a method for screening compounds to identify compounds that inhibit coagulase-negative staphylococci binding to host molecules. In accordance with the method, the compound of interest is combined with one or more of the SdrF, SdrG, or SdrH proteins or fragments thereof and the degree of binding of the protein to fibrinogen or other extracellular matrix proteins is measured or observed. If the presence of the compound results in the inhibition of protein-fibrinogen binding, for example, then the compound may be useful for inhibiting coagulase-negative staphylococci *in vivo* or *in vitro*. The method could similarly be used to identify compounds that promote interactions of coagulase-negative staphylococci with host molecules.

The method is particularly useful for identifying compounds having bacteriostatic or bacteriocidal properties.

For example, to screen for coagulase-negative staphylococci agonists or antagonists, a synthetic reaction mixture, a cellular compartment (such as a membrane, cell envelope or cell wall) containing one or more of the SdrF, SdrG, or SdrH proteins, or fragments thereof, such as consensus or variable sequence amino acid motifs, and a labeled substrate or ligand of the protein is incubated in the absence or the presence of a compound under investigation. The ability of the compound to agonize or antagonize the protein is shown by a decrease in the binding of the labeled ligand or decreased production of substrate product. Compounds that bind well and increase the rate of product formation from substrate are agonists. Detection of the rate or level of production of product from substrate may be enhanced by use of a reporter system, such as a colorimetric labeled substrate converted to product, a reporter gene that is responsive to changes in SdrF, SdrG, or SdrH nucleic acid or protein activity, and binding assays known to those skilled in the art. Competitive inhibition assays can also be used.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a SdrF, SdrG, or SdrH nucleic acid molecules or proteins or portions thereof, such as consensus or variable sequence amino acid motifs, and thereby inhibit their activity or bind to a binding molecule (such as fibrinogen) to prevent the binding of the SdrF, SdrG, or SdrH nucleic acid molecules or proteins to its ligand. For example, a compound that inhibits SdrF, SdrG, or SdrH activity may be a small molecule that binds to and occupies the binding site of the SdrF, SdrG, or SdrH protein, thereby preventing binding to cellular binding molecules, to prevent normal biological activity. Examples of small molecules include, but are not limited to, small organic molecules, peptides or peptide-like molecules. Other potential antagonists include antisense molecules. Preferred antagonists include compounds related to and variants or derivatives of SdrF, SdrG, or SdrH proteins or portions thereof, such as consensus or variable sequence amino acid motifs.

The nucleic acid molecules described herein may also be used to screen compounds for antibacterial activity.

X. Detection Kits for Coagulase-Negative Staphylococci

The invention further contemplates a kit containing one or more *sdrF*, *sdrG*, or *sdrH*-specific nucleic acid probes, which can be used for the detection of coagulase-negative staphylococci or coagulase-negative staphylococcal Sdr proteins or portions thereof, such as consensus or variable sequence amino acid motifs, in a sample or for the diagnosis of coagulase-negative staphylococcal infections. Such a kit can also contain the appropriate reagents for hybridizing the probe to the sample and detecting bound probe.

In an alternative embodiment, the kit contains antibodies specific to one or more SdrF, SdrG, or SdrH protein or peptide portions thereof, such as consensus or variable sequence amino acid motifs, which can be used for the detection of coagulase-negative staphylococci.

In yet another embodiment, the kit contains one or more SdrF, SdrG, or SdrH-proteins, or active fragments thereof, which can be used for the detection of coagulase-negative staphylococci organisms or antibodies to coagulase-negative staphylococcal Sdr proteins in a sample.

The kits described herein may additionally contain equipment for safely obtaining the sample, a vessel for containing the reagents, a timing means, a buffer

for diluting the sample, and a colorimeter, reflectometer, or standard against which a color change may be measured.

In a preferred embodiment, the reagents, including the protein or antibody, are lyophilized, most preferably in a single vessel. Addition of aqueous sample to the vessel results in solubilization of the lyophilized reagents, causing them to react. Most preferably, the reagents are sequentially lyophilized in a single container, in accordance with methods well known to those skilled in the art that minimize reaction by the reagents prior to addition of the sample.

EXAMPLES

The following examples are included to demonstrate preferred embodiments of the present invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventors to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1

Identification of Sdr encoding genes in coagulase negative staphylococci

Five genes (*clfA, clfB, sdrC, sdrD, sdrE*) have been identified in *Staphylococcus aureus* that contain the dipeptide aspartic acid and serine (DS), encoded by an 18 bp repeat motif GAY TCN GAY TCN GAY AGY, where Y = pyrimidines and N = any base. This family of proteins has been named the Sdr's for serine-aspartic acid repeat. All of the 5 *S. aureus sdr* genes encode proteins that contain features that characterize them as surface associated proteins in Gram positive bacteria; namely at the N-terminus there is a secretory signal and at the C-terminus there are (i) several positive charged residues that serve as a stop signal for protein secretion, (ii) a hydrophobic transmembrane region and (iii) a wall-spanning region with an LPXTG motif that is required for accurate sorting and correct protein orientation in the cell wall. To identify novel genes that encode cell surface proteins in coagulase negative staphylococci we used the DS coding region of *clf*A as a gene probe to determine if homologs exist within various coagulase negative

staphylococcal species. The coagulase negative staphylococcal species that we characterized were (1) *S. lugdunensis,* (2) *S. haemolyticus,* (3) *S. schleiferi* and (4) *S. epidermidis.* Each strain is listed below.

Ten strains each of *S. epidermidis, S. lugdunensis, S. schleiferi* and *S. haemolyticus* were obtained from Jerome Etienne (Lyon, France). In addition, Dr. Timothy Foster's strain collection contained *S. epidermidis* strains donated from other researchers. Southern hybridization analysis using genomic DNA isolated from all coagulase-negative staphylococcal strains was performed. Chromosomal DNA was cleaved with *Hin*dIII and the DS coding region of *clfA* was DIG-labeled (Boehringer) and used as a probe. Southern hybridization analysis of all ten *S. lugdunensis* strains revealed that a single *Hin*dIII fragment, of 9 kb, hybridized to the DS coding region of *clfA.* Analysis of *S. haemolyticus* strains with the DS-coding sequence of *clfA* revealed different sized fragments. Out of the ten strains tested, six strains gave a strongly hybridizing band between 18 kb and 10 kb. The possibility exists that more than one DS coding region is present on the *Hin*dIII fragment. After longer exposure of the autoradiogram, the four remaining strains showed weak hybridization to the DS coding region of *clf*A. The *clf*A probe did not detect a DS coding region in the genomic DNA from *S. schleiferi.* All *S. epidermidis* strains characterized revealed at least two *Hin*dIII fragments that hybridized to the DS coding region of *clfA.*

Strains tested:

<u>*S. lugdunensis* strains</u>

1. *S. lugdunensis* N940113
2. *S. lugdunensis* N940164
3. *S. lugdunensis* N940135
4. *S. lugdunensis* N950232
5. *S. lugdunensis* N920143
6. *S. lugdunensis* N930432
7. *S. lugdunensis* N940084
8. *S. lugdunensis* N940025
9. *S. lugdunensis* N910319
10. *S. lugdunensis* N910320

S. epidermidis strains

1. *S. epidermidis* ATCC1499O (Kloos)
2. *S. epidermidis* KH11
3. *S. epidermidis* K28
4. *S. epidermidis* TU3298
5. *S. epidermidis* 9142
6. *S. epidermidis* 1457
7. *S. epidermidis* 8400
8. *S. epidermidis* RP62a
9. *S. epidermidis* N910102
10. *S. epidermidis* N910173
11. *S. epidermidis* N910191
12. *S. epidermidis* N910231
13. *S. epidermidis* N910249
14. *S. epidermidis* N910275
15. *S. epidermidis* N950190
16. *S. epidermidis* N950329
17. *S. epidermidis* N910308
18. *S. epidermidis* N910160

S. haemolyticus strains

1. *S. haemolyticus* N97061
2. *S. haemolyticus* N960512
3. *S. haemolyticus* N910106
4. *S. haemolyticus* N91024
5. *S. haemolyticus* N920160
6. *S. haemolyticus* N910287
7. *S. haemolyticus* N92018
8. *S. haemolyticus* N930100
9. *S. haemolyticus* N950252
10. *S. haemolyticus* N93016

S. schleiferi strains

1. *S. schleiferi* JCM7430
2. *S. schleiferi* N920247
3. *S. schleiferi* N910245
4. *S. schleiferi* N910017
5. *S. schleiferi* N960518
6. *S. schleiferi* N950242
7. *S. schleiferi* N920162
8. *S. schleiferi* N92017
9. *S. schleiferi* N930047
10. *S. schleiferi* N920260

sdrF homologues in other *S. epidermidis* strains

17 strains of *S. epidermidis* were examined for the presence of the *sdrF* gene by Southern hybridization. Chromosomal DNA of the individual strains was cleaved with *Hin*dIII and probed with a region A coding sequence of *sdrF* as a probe. This DNA probe was DIG-labeled by PCR using pC5 (described further below in Example 2) as a template. The *sdrF* gene was present on a *Hin*dIII fragment that varied from 4-10 kb and was present in 12 out of 16 strains tested. Using the region R coding sequence of *clfA* as a probe also identified a band of the same size indicating that *sdrF* homologues in other *S. epidermidis* strains also contain region R coding sequence.

sdrG homologues in other *S. epidermidis* strains

16 strains of *S. epidermidis* were tested for the presence of the *sdrG* gene using a probe designed to the region A coding sequence of *sdrG*. Southern hybridization analysis revealed that *sdrG* was present on a 16 kb *Hin*dIII fragment and was present in all *S. epidermidis* strains examined. The primer sequence used for amplification of region A coding sequence of *sdrG* is as follows:

F1-*sdrG*: 5' GATGATGAATTATCAGAC 3' (SEQ ID No. 21)

R.-*sdrG*: 5' CAGGAGGCAAGTCACCTTG 3' (SEQ ID No. 22)

(encompassing coordinates 195 to 1795 of *sdrG*)

DS-coding region homologues in *S. epidermidis* strains

Chromosomal DNA was cleaved with *Hin*dIII and the DS-coding region of *clfA* was DIG labeled (Boehringer) and used a probe. Southern hybridization analysis revealed at least two *Hin*dIII fragments that hybridized to the DS-coding region of *clfA*. Ten strains hybridized to three *Hin*dIII fragments.

Example 2

Studies of the Sdr genes in coagulase negative staphylococci, and identification, isolation, sequencing and expression of SdrF, SdrG and SdrH

OVERVIEW

Staphylococcus epidermidis strains can express three different cell surface-associated proteins that contain serine-aspartate dipeptide repeats. Proteins SdrF and SdrG are similar in sequence and structural organization to the Sdr proteins of *S. aureus.* They comprise 625 and 548 residue unique region As at their N termini, respectively, followed by a variable number of 110-119 residue region B repeats, an SD repeat region, and C-terminal LPXTG motifs and hydrophobic domains characteristic of surface proteins that are covalently anchored to peptidoglycan. In contrast, SdrH has a short 60 residue region A at the N terminus, followed by a SD repeat region, a unique 277 residue region C, and a C-terminal hydrophobic domain. SdrH lacks an LPXTG motif. DNA encoding each region A of SdrF, SdrG and SdrH was cloned into expression vectors in *E. coli*, and recombinant protein was expressed and purified. Specific antisera were raised in rabbits and used to identify the Sdr proteins expressed by *S. epidermidis.* Only SdrF was released from lysostaphin-generated protoplasts of cells grown to late exponential phase. SdrG and SdrH remained associated with the protoplast fraction and were thus not sorted and linked to peptidoglycan. In Southern hybridization analyses, the *sdrG* and *sdrH* genes were present in all sixteen strains tested, while *sdrF* was present in twelve strains. Antisera from fifteen patients that had recovered from *S. epidermidis* infections contained antibodies that reacted with recombinant region As of SdrF, SdrG and SdrH, suggesting that these proteins are expressed during infection.

BACKGROUND

S. epidermidis is a common inhabitant of human skin and a frequent cause of foreign-body infections. Pathogenesis is facilitated by the ability of the organism to first adhere to, and subsequently form biofilms on, indwelling medical devices such as artificial valves, orthopedic devices, and intravenous and peritoneal dialysis catheters. Device-related infections jeopardize the success of medical treatment and significantly increase patient morbidity (11).

Adherence of *S. epidermidis* to synthetic surfaces has been correlated with both surface hydrophobicity and cell-surface proteins. (2, 13). Protease treatment of *S. epidermidis* has been shown to reduce hydrophobicity and adherence (24), and a monoclonal antibody reactive to a 220 kDa cell-surface protein of *S. epidermidis* was able to partially block bacterial attachment to polystyrene (30). Polysaccharide expressed by the *ica* operon is crucial in formation of biofilm. One group suggested that the polysaccharide adhesin (PS/A) is sufficient for both adhesion and cell-cell interaction associated with the accumulation phase of biofilm formation. Another view is that adherence is mediated by a surface-associated protein while the polysaccharide is responsible only for the accumulation phase (5, 12, 19).

Like *S. epidermidis*, *S. aureus* can also adhere to medical-implant devices but this attachment is predominantly mediated by bacterial receptors specific for host fibrinogen and fibronectin that coat biomaterial surfaces shortly after implantation. *S. aureus* adhesins that mediate these interactions include the fibrinogen-binding proteins, ClfA and ClfB, and the fibronectin-binding proteins, FnbpA and FnbpB [reviewed in (3)]. Although *S. epidermidis* has the potential to interact with fibrinogen, fibronectin, vitronectin, and laminin (6, 25, 29), little is known of the specific adhesins mediating these interactions or of how these interactions influence bacterial adherence to biomaterials coated with host proteins.

The fibrinogen-binding clumping factor protein (or ClfA) of *S. aureus* (Fig. 1A) is distinguished by the presence of a serine-aspartate (SD) dipeptide repeat region (referred to as region R in previous studies) located between a ligand-binding region A and C-terminal sequences and associated with attachment to the cell-wall (16, 17). The SD-repeat region is predicted to span the cell wall and extend the ligand-binding region from the surface of the bacteria (4). ClfA is the predecessor of a SD-repeat (Sdr) protein family found in *S. aureus*. Additional members include ClfB (a second fibrinogen-binding clumping factor), SdrC, SdrD, and SdrE (Fig. 5A) (8, 21). SdrC,

SdrD, and SdrE proteins contain additional repeats, termed region B repeats, located between the region A and SD repeats. Each B repeat is 110-113 amino acids in length and contains a putative Ca^{2+}-binding, EF-hand motif. Ca binding has been shown to be required for the structural integrity of the region B repeats (9). The functions of SdrC, SdrD, and SdrE are unknown, but the proteins are hypothesized to interact with host matrix molecules *via* their region As.

This example describes three Sdr proteins expressed by *S. epidermidis*. Two have sequence similarity to, and the same structural organization, as the Sdr proteins of *S. aureus,* while SdrH is distinct. The genes encoding these proteins are prevalent among *S. epidermidis* strains. The presence of antibodies reactive to each Sdr region A in convalescent patient antisera suggest that the proteins are expressed during infection.

MATERIALS AND METHODS

Bacterial strains and growth conditions.

E. coli XL-1 Blue or JM109 were used as recombinant host strains. Strains XL-1 Blue or TOPP 3 (Stratagene, La Jolla, CA) cells were used for protein expression. Bacteria were routinely grown in Luria broth or agar (Gibco BRL, Gaithersburg, MD) supplemented with 100 $\mu g\ ml^{-1}$ ampicillin (USB, Cleveland, OH). *S. epidermidis* strains (Table 2) were grown in tryptic soy broth (TSB) or agar (TSA) (Difco, Detroit, MI).

Cloning and sequencing of the *sdr* genes

The *sdrF* gene was cloned from *S. epidermidis* strain 9491. *Hin*dIII-DNA fragments ranging from 6.5 to 7.5 kb in length were isolated from an agarose gel and ligated into a pBluescript SK+ cloning vector (Stratagene) digested with *Hin*dIII and treated with calf-intestine alkaline phosphatase (CIAP) (Promega, Madison, WI). One recombinant plasmid, pC5, was identified by PCR screening (27) with primers directed toward DNA encoding the SD-repeat region of ClfA (P3 and P4 primers, Table 3).

The *sdrG* gene was cloned from a λGem®-11 library of *S. epidermidis* strain K-28 generated with DNA that had been partially digested with *Sau*3A and ligated into the half-site *Xho*I arms of λGem®-11 (Promega). After packaging, a positive

phage, designated E6-2, was identified by hybridization of a DNA probe representing the ClfA SD-repeat region. A *Sac*I-*Kpn*I DNA fragment from E6-2 was then subcloned into the *E. coli* plasmid vector, pZero (Invitrogen, Carlsbad, CA). This clone was then mapped with restriction endonucleases, and a 3.5 kb *Eco*RI-*Kpn*I fragment containing DNA with homology to that encoding SD-repeat amino acids sequence was subcloned into pUC18 (Amersham Pharmacia Biotech, Piscataway, NJ) to create pE6-2.

The *sdrH* gene was cloned as follows. *Hin*dIII fragments obtained from *S. epidermidis* strain 9491 genomic DNA were size fractionated on a 5-20% sucrose gradient. DNA from fractions containing 1.5-2.5 kb fragments were ligated into pBluescript digested with *Hin*dIII and dephosphorylated with CIAP (Promega). *E. coli* transformants containing the ligated products were screened by colony-blot hybridization with a DIG-labeled (Boehringer Mannheim, Indianapolis, IN) probe made to DNA encoding the ClfA SD-repeat region.

Automated dideoxy-DNA sequencing was performed on both strands of cloned DNA. In most cases, extension of DNA sequence on a given clone was achieved with primer walking. This method, however, could not cover the length of repeat DNA encoding the SD-repeats of SdrF. Therefore, this region of DNA was excised from pC5 with Sau3A, ligated into pBluescript, and used as a template for the construction of exonuclease deletion derivatives (Erase-a-base System, Promega). Appropriate deletions on both strands (not shown) were identified by PCR screening and restriction mapping.

Table 2. *S. epidermidis* strains used in this study

Strains	Comments and properties	Source or reference
9491	SdrF and SdrH prototype strain	ATCC strain
ATCC14990	Reference strain	W. Kloos
KH11		P. Vaudaux
K28	SdrG prototype strain	P. Vaudaux
RP62a		
TU3298	Transformable strain	F. Gotz
9142	Biofilm former	D. Mack
1457		D. Mack
8400		
N910308	Reference strain, Lyon, France	J. Etienne
N910160	Reference strain, Lyon, France	J. Etienne
N910102	Reference strain, Lyon, France	J. Etienne
N910173	Reference strain, Lyon, France	J. Etienne
N910191	Reference strain, Lyon, France	J. Etienne
N910231	Reference strain, Lyon, France	J. Etienne
N910249	Reference strain, Lyon, France	J. Etienne

Table 3. Primers used in PCR amplification for DNA probes and protein expression constructs

Regions amplified	Sequence	Vector destination	Template DNA
clfA SD repeat	F: GCCGGATCCCCAATTCCAGAGGATTCA (SEQ ID No. 23) R: GCCAAGCTTATTGTTAGAACCTGACTC (SEQ ID No. 24)	Na	pCF48
SD repeats	P3: GATTCAGATAGCCATTC (SEQ ID No. 25) P4: CTGAGTCACTGTCTGAG (SEQ ID No. 26)	Na	*sdr* clones
sdrF region A	F: CCCGGATCCGCTGAAGACAATCAATTAG (SEQ ID No. 27) R: CCCAAGCTTAATTATCCCCCTGTGCTG (SEQ ID No. 28)	pQE30	strain 9491
sdrG region A	F: CCCGGATCCGAGGAGAATACAGTACAAGACG (SEQ ID No. 29) R: CCCGGTACCTAGTTTTTCAGGAGGCAAGTCACC (SEQ ID No. 30)	pQE30	strain K28
sdrH full length	F: CCCGGATCCGAAGGTAATCATCCTATTGAC (SEQ ID No. 31) R: CCCAAGCTTACTTTTTTCTTCTAAAGATATATAGTCC (SEQ ID No. 32)	pQE30	strain 9491
sdrF region A	F: same as above R: CCCGAATTCAATTATCCCCCTGTGCTGTTG (SEQ ID No. 33)	pGEX-2T	strain 9491
sdrG region A	F: same as above R: CCCGAATTCTAGTTTTTCAGGAGGCAAGTCACC (SEQ ID No. 34)	pGEX-2T	strain K28
sdrH region A	F: GGCGGATCCGAAGGTAATCATCCTATTG (SEQ ID No. 35) R: GGCAAGCTTCTAAATATGTGTCATTTTC (SEQ ID No. 36)	pGEX-KG	strain 9491

na: not applicable
underline: restriction endonuclease site used for cloning

Southern hybridizations

Southern blot transfers and hybridizations have been described elsewhere (8). DNA probes were made from PCR products encoding the SD-repeat region of ClfA or each region A of SdrF, SdrG, and SdrH (Table 3). PCR products were generated with Taq DNA polymerase (Gibco BRL), and probes were digoxigenin (Boehringer Mannheim) or fluorescein (Amersham) labeled.

Protein expression and purification for antisera production

DNA encoding recombinant SdrF, SdrG, or SdrH region A was obtained by PCR amplification of genomic template DNA from *S. epidermidis* strains 9491 or K28 with appropriate primers (Table 3). The SdrF region A construct lacked the terminal residue, proline. PCR utilized Pfu DNA polymerase (Stratagene); specifications have been previously described (7). PCR products were digested with appropriate restriction endonucleases and ligated into the expression vectors pQE30 (Qiagen, Valencia, CA) to generate histidine-tagged proteins, or pGEX-2T (Pharmacia) or pGEX-KG to generate GST-tagged proteins. Proteins were expressed in *E. coli* by growing 4 liters of recombinant organisms to an optical density (OD_{600}) of 0.5 and inducing with 0.3 mM isopropyl-1-thio-β-D-galactoside (IPTG) (Gibco BRL) for two hours. The cells were harvested in PBS (150 mM NaCl, 4.3 mM Na_2HPO_4, 1 mM NaH_2PO_4) and frozen at -80 °C. *E. coli* were passed through a French press and the supernatants of these lysates were filtered through a 0.45 μm membrane. Soluble histidine-tagged proteins, present in the supernatants, were initially purified by metal-chelating chromatography. The supernatants were applied to a 5 ml Ni^{2+}-charged HiTrap chelating column (Pharmacia Biotech Inc.) and bound proteins were eluted with 200 ml linear gradients of 0-200 mM imidazole in 4 mM Tris-HCl, 100 mM NaCl, pH 7.9 at a flow rate of 5 ml/min. Fractions containing recombinant proteins were identified by SDS-PAGE (see below), pooled, and dialyzed against 25 mM Tris-HCl, pH 8.0. Dialyzed proteins were concentrated and further purified by ion-exchange chromatography by applying the samples to a 5 ml HiTrap Q column (Pharmacia Biotech Inc.) and eluting bound proteins with 200 ml linear gradients of 0-0.5 M NaCl in 25 mM Tris-HCl, pH 8.0 at a flow rate of 5 ml/min. Fractions containing purified recombinant proteins were identified by SDS-PAGE. GST-tagged proteins were purified from *E. coli* lysates obtained as described above. Lysates were passed

through 10 ml glutathione-agarose columns under gravity flow and washed with five column volumes of PBS. Proteins were eluted from the columns with freshly prepared 5 mM reduced glutathione (Sigma) in 50 mM Tris-HCl, pH 8.0. Purified proteins were used to raise antisera in New Zealand White rabbits using standard protocols issued by HTI Bioproducts (Romano, CA) or by the Biological Core Facility at the National University of Ireland (Dublin, Ireland).

SDS-PAGE and Western blot transfer

SDS-PAGE utilized trycine gels containing 10% acrylamide (28). Separated proteins were transferred to PVDF membrane (Immobilon-P, Millipore, Bedford, MA) with a semi-dry transfer cell (Bio-Rad Laboratories, Hercules, CA). All protein samples were heat denatured under reducing conditions. Purified proteins (1 μg each) were subjected to SDS-PAGE and stained with Coomassie brilliant blue. *E. coli* lysates or lysate fractions were obtained as follows: IPTG induced, recombinant *E. coli* were grown to an OD_{600} of 2.0, washed and resuspended to original volume in PBS and prepared for SDS-PAGE. 10 μl of each preparation was loaded into individual wells of acrylamide gels. *S. epidermidis* strains were grown to early stationary phase in TSB containing 1.25 U per 10 ml of the endoproteinase inhibitor α2-Macroglobulin (Boehringer Mannheim). The cells were adjusted to an OD_{600} of 2, washed, and resuspended in one half the original volume. Protease inhibitors (4 mM phenylmethylsulphonyl fluoride, 1 mM N-ethyl-maleimide, and 25 mM aminohexanoic acid) and DNAse (10 μg ml^{-1}) were added prior to lysostaphin (100 μg ml^{-1}) and lysozyme (100 μg ml^{-1}). Enzymatic digestions were performed for 30 min. at 37 °C with shaking. Separation of cell-wall proteins from protoplasts utilized the same conditions in the presence of 30% raffinose. *S. epidermidis* lysates or lysate fractions were treated as those for *E. coli* and 30 μl aliquots of samples were placed into wells of acrylamide gels.

Immunoassays

Western immunoassays were performed as follows: Western blots were incubated in PBS containing 1% non-fat dry milk for 1 hr. The blots were then incubated with antisera (diluted in PBS-milk) for 1 hr. Monoclonal, anti-histidine antibody (Clonetech, Palo Alto, CA) was diluted to 1:3000. Anti-SdrFA antisera

(immune, preimmune, and antigen-absorbed) were diluted to 1:30,000; anti-SdrGA antisera were diluted to 1:2000, and anti-SdrHA antisera were diluted to 1:1000. Antisera absorptions have been previously described (14). Briefly, anti-SdrFA and anti-SdrGA antisera were extensively absorbed, respectively, with GST-tagged SdrGA and SdrFA proteins present in insoluble fractions of induced *E. coli* that had been sonicated and then centrifuged. This procedure was used to remove potential cross-reactive antibodies present in each antiserum. Removal of immunoreactive anti-SdrFA, -SdrGA, and -SdrHA antibodies was accomplished by absorbing each antiserum with *E. coli* lysates containing, respectively, GST-tagged SdrFA, SdrGA, and SdrHA. Following antisera incubation, Western blots were washed three times with PBS and incubated with a 1:2000 dilution of goat, anti-rabbit or anti-mouse IgG conjugated to alkaline phosphatase (Bio-Rad Laboratories) for 30 min. The blots were then washed and developed in chromogenic substrate (150 μg ml^{-1} 5-bromo-4-chloro-3-indolyl phosphate p-toluidine salt and 300 μg ml^{-1} p-nitro blue tetrazolium chloride in bicarbonate buffer) (Bio-Rad) for 10-15 min.

Reactivity of convalescent patient IgG to recombinant proteins has been previously described (1). Antisera from fifteen individuals recovering from *S. epidermidis* infections were collected and IgG was purified using protein-A sepharose chromatography. An enzyme-linked immunosorbent assay (ELISA) was used to demonstrate reactivity of IgG (2 μg per well) to recombinant proteins (1 μg per well of histidine-tagged SdrFA or SdrGA, or GST-tagged SdrHA) coated on microtiter plates.

RESULTS

Identification of the *sdrF*, *sdrG*, and *sdrH* genes.

Preliminary Southern hybridization analysis of *S. epidermidis* DNA revealed the presence of several loci hybridizing with DNA encoding the SD repeats of the *S. aureus* Sdr protein family (unpublished observations). To further define these loci, we cloned three DNA fragments from *S. epidermidis* strains 9491 and K28. Two clones, pC5 and pC28, were obtained from strain 9491 by direct ligation of *Hin*dIII-DNA fragments into *E. coli* plasmid vectors. A third clone, E6-2, was obtained from a λGem®-11 genomic library made from strain K28. A segment of the E6-2 insert DNA was subcloned into an *E. coli* plasmid vector to form pE6-2. pC5, pE6-2, and pC28

were found to have 6.8, 6.0, and 2.0 kb DNA inserts, respectively (not shown).

DNA sequence analysis revealed the presence of single open reading frames (ORF) in each plasmid. The ORFs, designated *sdrF*, *sdrG*, and *sdrH*, were 5199, 2793, and 1461 base pairs (bp) in length, respectively. A leucine, rather than a methionine, codon is predicted to act as a translational start codon for *sdrG*. A potential ribosome binding site (GGAG) (SEQ ID No. 37) was identified 7-12 bp 5' of each ORF. DNA sequences of 500-1000 bp flanking the *sdrF*, *sdrG*, and *sdrH* ORFs were not similar, suggesting that they are not tandemly linked like the *sdrC*, *sdrD*, and *sdrE* genes of *S. aureus* (data not shown).

The deduced amino acids sequences of SdrF, SdrG, and SdrH.

The amino acid structural organization of the *S. epidermidis* SdrF and SdrG proteins are similar to the *S. aureus* Sdr proteins and thus have features typical of cell-surface proteins that are covalently anchored to the peptidoglycan of Gram-positive bacteria. These cell-surface features include positively-charged residues at the extreme C terminus preceded by a hydrophobic membrane spanning region, and an LPXTG (SEQ ID No. 17) motif. The SD repeat regions are located N-terminal of the LPXTG (SEQ ID No. 17) motif and are proposed to traverse the cell wall (4, 10). SdrF and SdrG contain predicted signal sequences at their N-termini (52 and 50 residues, respectively) and residues associated with cell wall linkage at their C-termini (Fig. 5B, 5C). The SD-repeat regions of SdrF and SdrG (see below) end seven and thirteen residues, respectively, proximal to the LPXTG motifs. The SD-repeat regions of SdrF and SdrG contain 558 and 56 residues, respectively (Fig. 5B). The dipeptide composition of SdrG does not diverge from serine and aspartate, whereas in SdrF, 26 alanine residues occur within the SD-repeat region. The predicted molecular masses of the mature proteins (with loss of the signal sequences) are 179 kDa for SdrF and 97.6 kDa for SdrG.

The Sdr proteins of *S. aureus* each possess a structurally distinct, known or putative ligand-binding domain at their N terminus called region A (8, 16, 21). The N termini of mature SdrF and SdrG possess 625 and 548 amino acid region As, respectively. Pairwise comparisons reveal that the amino acid sequences of SdrF and SdrG region As are 22% identical to each other and 20-35% (mean=23%) identical to the region As of the *S. aureus* Sdr proteins.

Amino acid sequence motifs have been reported in the region As of *S. aureus*

Sdr proteins, and these include a putative Ca^{2+}-binding EF-hand motif in ClfA, a cation-coordinating MIDAS motif in ClfB, and a common Sdr protein motif, TYTFTDYVD (SEQ ID No. 16), of unknown function (8, 23). The region As of SdrF and SdrG both contain a TYTFTDYVD (SEQ ID No. 16) motif, and an EF-hand motif (DYSEYEDVTNDDY) (SEQ ID No. 38) was found in the region A of SdrG.

Three Sdr proteins of *S. aureus* (SdrC, SdrD, and SdrE) contain variable numbers of 110-113 amino acid segments called region B repeats (Fig. 5A), and each repeat contains a putative Ca^{2+}-binding EF-hand motif (8, 9). Likewise, SdrF contains four region B repeats (of 119, 110, 111, and 111 residues), and SdrG contains two region B repeats (of 113 and 111 residues) (Fig. 5B). Each repeat contains a putative EF-hand motif with a consensus sequence of DX(N/D)X(D/N)GXX(D/N/G)XX(E/D). The region B repeats of SdrF and SdrG have 43-85% (mean=55%) identity with each other and 39-73% (mean=54%) identity to the region B repeats found in the *S. aureus* Sdr proteins.

The structural organization of SdrH at the amino acid sequence level is considerably different than that of SdrF and SdrG. Following a potential 30 residue signal sequence at its N terminus, SdrH has a unique 60 residue stretch (region A) followed by a 120-residue SD-repeat region and a 277-residue segment, region C, that contains a hydrophobic sequence at its C terminus but lacks an appropriately placed LPXTG motif. The sequence LGVTG, however, occurs within the hydrophobic region. (Fig. 1B, 1C). SdrH contained no region B repeats. The region A and region C of SdrH have no amino acid sequence similarities with other known Sdr proteins or protein sequences from various databases. Motifs common to other Sdr proteins were not found. The mature molecular mass of SdrH is predicted to be 50.5 kDa.

Together, these result suggest that *S. epidermidis* has the capacity to express two proteins related to the *S. aureus* Sdr protein family, as well as a third Sdr protein with novel structure.

Distribution of *sdrF, sdrG, and sdrH* in *S. epidermidis* strains.

In Southern hybridization analysis, a DNA probe representing the encoding region of the ClfA SD-repeats hybridized to several genomic *Hin*dIII fragments in sixteen *S. epidermidis* strains (Fig. 6A). Three hybridizing fragments were observed in most strains, presumably representing the *sdrF*, *sdrG*, and *sdrH* genes. To confirm

this and determine the frequency of the genes within these strains, additional analyses were performed with probes specific for DNA encoding each region A. The *sdrH* probe hybridized to fragments between 1.8-6.5 kb in all strains (Fig. 6B). The *sdrG* probe hybridized to a 16-kb fragment in all strains examined (Fig. 6C). In addition, the probe hybridized to *Hin*dIII fragments of 3.4 kb in four of the sixteen strains (KH11, K28, RP62a, and N910102). The same 3.4 kb fragments, however, did not hybridize with a probe specific for DNA encoding SD-repeats (Fig. 6A), suggesting the presence of a gene with similarity to the *sdrG* region A that lacks a SD-repeat region. Figure 6D shows a Southern blot probed with both *sdrG* and *sdrF* region A DNA. The *sdrF* probe hybridized to *Hin*dIII-DNA fragments between 4.5 kb and 10 kb in twelve out of sixteen strains (strains K28, RP62a, N910173, and N910191 lacked a hybridizing band). These results suggest that the *sdrF*, *sdrG*, and *sdrH* genes are prevalent in *S. epidermidis* strains.

Expression of SdrF, SdrG, and SdrH in *S. epidermidis*.

Immunologic methods were used to determine if SdrF, SdrG, and SdrH are expressed by *S. epidermidis*. Specific rabbit antisera were raised to recombinant fusion proteins representing different region As (designated SdrFA, SdrGA, and SdrHA). SdrFA and SdrGA were fused to polyhistidine (His_n), and SdrHA was fused to GST (Fig. 7A). Monospecificity of the antisera was confirmed against a panel of recombinant proteins containing different protein fusions. Specifically, antisera raised to His_n-SdrFA and -SdrGA did not, respectively, cross react with GST-SdrGA and -SdrFA (Fig. 7B). In addition, these same antisera did not cross react to GST-SdrHA (Fig. 7B). Antiserum raised to GST-SdrHA reacted to a full-length, His_n-SdrH protein but not to His_n-SdrFA or -SdrGA proteins (Fig. 7C).

The region A-specific antisera were used to identify native SdrF, SdrG, and SdrH in lysates of their cognate *S. epidermidis* strains by Western immunoblotting. The anti-SdrFA antiserum reacted with a ca 230 kDa band from strain 9491 (Fig. 8A). This band was not present with Western blots reacted with preimmune antiserum or with anti-SdrFA antiserum that had been absorbed with *E. coli* lysates expressing a GST-SdrFA fusion protein (Fig. 8A). The anti-SdrGA antiserum reacted to a 170 kDa band in a lysate of *S. epidermidis* strain K28. This band was not present with preimmune antiserum or with anti-SdrGA antiserum that had been absorbed with an *E. coli* lysate expressing a GST-SdrGA fusion protein (Fig. 8B).

Antiserum to SdrHA recognized a 75 kDa band in strain 9491, and this reactivity could be removed by absorbing the antiserum with recombinant SdrH present in an *E. coli* lysate (Fig. 8C). The apparent molecular masses of the anti-SdrFA, -SdrGA, and -SdrHA immunoreactive bands are larger than the masses predicted from the deduced amino acid sequences (179, 97, and 50 kDa, respectively). Decreased migration on SDS-PAGE has been previously noted for two *S. aureus* Sdr proteins, ClfA and ClfB, where up to a 50-100% increase in predicted mass was observed. The acidic nature of the Sdr proteins has been suggested to account for these observations.

Differences in molecular mass of SdrH in *S. epidermidis* strains.

Western immunoblot analysis, different strains of *S. epidermidis* possessed SdrH with apparent molecular masses that varied between 60 and 75 kDa (Fig. 9A). Variations in the molecular mass of ClfA has been previously correlated with the length of the SD-repeat region (15). PCR analysis of the *sdrH* genes from the *S. epidermidis* strains used above revealed that variations in the size of DNA encoding the SD-repeat regions correlated with the different masses of the SdrH proteins on Western blots. In contrast, PCR products of DNA encoding the region C of each SdrH were similar in size (Fig. 9B).

Analyses of SdrF, SdrG, and SdrH in cell wall extracts and protoplasts.

The presence of a LPXTG motif in both SdrF and SdrG suggests that these proteins are anchored in the cell wall and would therefore be present in cell-wall extracts of lysostaphin-treated *S. epidermidis*. Western blot analyses of early stationary phase, lysostaphin-digested *S. epidermidis* strain 9491 with anti-SdrFA antiserum revealed the presence of the 230 kDa SdrF band in both the whole-cell lysate and the cell-wall extract but not in the protoplast fraction (Fig. 10A). In contrast, analysis of the same samples with anti-SdrGA antiserum revealed the presence of SdrG (170 kDa) in the lysate and protoplast fraction but not in the cell-wall extract (Fig. 10B). Similar results were observed with blots containing lysostaphin-treated strain K28 (not shown). Further analysis of 9491 lysostaphin fractions with anti-SdrHA antiserum revealed an immunoreactive band in both the cell-wall lysate and protoplast fraction (Fig. 10C). These results suggest that, under these *in vitro* conditions, SdrF is localized and anchored to the cell wall, and that

SdrG (despite its LPXTG motif) and SdrH are either associated with the cytoplasmic membrane or located inside the cell.

Reactivity of convalescent patient antisera to SdrF, SdrG, and SdrH.

Recently, IgG from patients recovering from *S. aureus* infections has been shown to react with the fibronectin binding protein (FnbpA), suggesting that FnbpA is expressed by *S. aureus* during infection (1). Here, IgG purified from the antisera of fifteen patients recovering from various *S. epidermidis* infections was tested by ELISA for reactivity with the recombinant SdrF, SdrG, and SdrH region A proteins. Figure 11 shows that IgG from patients' antisera had a higher titer to SdrFA, SdrGA, and SdrHA compared to that of IgG purified from pooled children antisera. The patients' IgG was often more reactive with SdrGA and SdrHA than with SdrFA. These results suggest that the Sdr proteins are expressed during *S. epidermidis* infection in humans.

DISCUSSION

S. epidermidis infections in humans are associated with foreign-body devices that become rapidly coated with matrix proteins when introduced into the patient (26). Although mechanisms (encoded by the *ica* operon) have been proposed to mediate adherence and biofilm formation on uncoated polymer surfaces, specific factors mediating adherence to surfaces coated with host proteins have been poorly defined. The presence of Sdr proteins in *S. epidermidis* suggest that *S. epidermidis* may bind protein-coated matrix devices in a manner similar to *S. aureus* which utilizes ClfA and ClfB to mediate adherence to prosthetic devices coated with fibrinogen (21, 31). In this regard, a recombinant protein, expressed from cloned *S. epidermidis* DNA and similar to SdrG, has been shown to bind fibrinogen (22).

The *S. epidermidis* Sdr proteins may play a role in pathogenic processes apart from initial adherence. Experiments showing that proteolytic cleavage of the fibronectin-binding protein, Fnbp, from the surface of *S. aureus* produces a soluble, active protein, and this cleavage has been proposed to initiate release and dissemination of *S. aureus* from solid-phase fibronectin (18). Analogously, native SdrF and SdrG undergo rapid degradation in *in vitro* culture conditions in the absence of protease inhibitors (unpublished observations), and this proteolysis may provide a mechanism by which the bacteria can be detached from a substrate.

SdrF fractionates with cell-wall anchored proteins released by lysostaphin digestion, suggesting that it is present on the cell surface. In contrast, SdrG, which contains an LPXTG, cell-wall sorting motif similar to SdrF, was found only in the protoplast fraction. The apparent lack of SdrG in the cell-wall fraction may be influenced by the bacterial growth phase or by proteolytic enzymes expressed during various growth phases. For instance, SdrG was found to be absent or diminished in lysates of strain K28 in early exponential phase. In addition, a number of *S. epidermidis* strains grown to late stationary phase did contain SdrG in the cell-wall extracts while other strains (including K28 and 9491) contained only potential degradation products of SdrG (unpublished results). Further studies are warranted to detail the regulation of SdrG anchorage to the cell wall and localization at the cell surface. Similarly, additional studies are required for SdrH, which contains features of cell-wall proteins but lacks a clear LPXTG motif.

As mentioned above, a protein similar to SdrG (designated Fbe) has been identified as a *S. epidermidis* protein capable of binding fibrinogen (22). Fbe was reported to have a region A directly adjacent to a SD-repeat region, but structures similar to region B repeats were not described. We have found that Fbe contains two region B repeats with 99% amino acids identity to the region B repeats of SdrG (unpublished results). In the reported sequence of Fbe, these repeats begin at amino acid 601 and end at the beginning of the SD-repeats. The original region A of Fbe was reported to contain a minimal fibrinogen-binding region between residues 269-599. With respect to the newly identified region B repeats, the minimal fibrinogen-binding region would be positioned at the extreme C terminus of region A. This is similar to ClfA which contains a minimal fibrinogen-binding region at its C terminus (McDevitt, 1995). The region As of Fbe and SdrG are 93% identical in amino acid sequence, and the predicted minimal-binding regions are 98% identical.

SdrH is unique among the eight described members of the Sdr protein family (from *S. aureus* and *S. epidermidis*) in that it possesses a divergent putative domain organization. The position of the SD-repeat region at the N terminus, a novel region C, and the lack of definitive cell-wall association sequences suggest that this protein functions differently than the known Sdr MSCRAMMs. Further studies on the bacterial localization and ligand-binding potential of SdrH are in progress.

The SD-repeat regions of SdrF and SdrG represent the longest and shortest SD repeats (558 and 56 residues, respectively) of the eight known Sdr proteins.

Although the SD-repeats do not participate in fibrinogen binding, wild-type levels of functional ClfA expression were found to require a SD-repeat region with more than 40 residues (72 residues from the end of region A to the LPXTG motif) (4). This expanse of amino acids was postulated to span the cell wall and present a functional region A. Although SdrG contains 73 residues from the end of the region B repeats to the LPXTG motif, the two region B repeats may also affect the structure and function of the ligand-binding region A. The purpose of an extremely large SD-repeat region in SdrF is unknown. Given the interaction of the SD-repeat region with the cell wall, the differences in length of the SD-repeat regions between SdrF and SdrG may be associated with the localization differences observed in cell-wall fractions of these proteins. Variations in the length of SD-repeats in SdrH have been described. The SdrH protein from strain KH11 (the smallest SdrH observed) was found by DNA sequence analysis to contain 64 residues (unpublished results). The role of the SD repeats in SdrH is unknown but we speculate that this region, like other Sdr proteins, may be partially associated with the cell wall.

Genes encoding Sdr proteins of *S. epidermidis* are present in most of the clinical isolates examined to date. These strains were isolated from a broad range of disease outcomes in patients of diverse geographic locations. In addition, patients recovering from a variety of *S. epidermidis* infections have SdrF-, SdrG-, and SdrH-reactive IgG in their antisera. Similar traits have been observed for the five reported Sdr proteins of *S. aureus* [(8, 17) and unpublished results]. These studies suggest that the Sdr proteins are important constituents in *S. epidermidis* infectivity and growth. Interestingly, loci with homology to DNA encoding SD-repeat regions are also prevalent in strains of *S. haemolyticus*, *S. lugdunensis*, and *S. intermedius*, additional staphylococci capable of producing disease in humans and other mammals (unpublished results).

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